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                    GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:         April 6, 2006, 20:33:55 ; Search time 770 Seconds
                                          (without alignments)
                               7621.839 Million cell updates/sec

Title:          US-10-659-983A-18
Perfect score:  1467
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters:    18535810

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published Applications NA_New:*
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     15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match Match%	Length	DB	ID	Description
1		1133.4	77.3	1522	11	US-11-198-242-2	Sequence 2, Appli
2		1131.8	77.2	1526	11	US-11-198-242-1	Sequence 5, Appli
3		1067.9	72.8	1405	9	US-10-515-311-5	Sequence 5, Appli
4		1018.8	69.4	1501	9	US-10-513-639-1	Sequence 1, Appli
5		1009	68.7	1510	9	US-10-831-286A-48682	Sequence 48682, A
6		1007.4	68.7	1510	9	US-10-831-286A-48680	Sequence 48680, A
7		1006.6	68.6	1508	9	US-10-831-286A-48684	Sequence 48684, A
8		1006.6	68.6	1508	9	US-10-831-286A-48685	Sequence 48685, A
9		1006	68.6	1507	9	US-10-831-286A-48677	Sequence 48677, A
10		995.8	67.9	1530	9	US-10-831-286A-48671	Sequence 48671, A
11		988.8	67.4	1535	9	US-10-831-286A-48678	Sequence 48678, A
12		984	67.1	1494	9	US-10-831-286A-48681	Sequence 48681, A
13		983.8	67.1	1527	9	US-10-831-286A-48693	Sequence 48693, A
14		982.4	67.0	1493	9	US-10-831-286A-48683	Sequence 48683, A
15		979.2	66.7	1494	9	US-10-831-286A-48676	Sequence 48676, A
16		979	66.7	1519	9	US-10-831-286A-48687	Sequence 48687, A
17		978.2	66.7	1542	5	US-09-941-095-158	Sequence 158, App
18		978.2	66.7	1542	11	US-11-198-746-158	Sequence 158, App
19		978.2	66.7	1542	11	US-11-198-794-158	Sequence 158, App
20		978.2	66.7	1542	11	US-11-198-657-158	Sequence 158, App
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22		975.4	66.5	1495	9	US-10-831-286A-48675	Sequence 48675, A
23		974.8	66.4	1494	9	US-10-831-286A-48669	Sequence 48669, A
24		971	66.1	1503	9	US-10-831-286A-48665	Sequence 48665, A
25		970	66.1	1514	9	US-10-831-286A-48666	Sequence 48666, A
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27		964.4	65.7	1486	9	US-10-831-286A-48679	Sequence 48679, A
28		964	65.7	1492	9	US-10-831-286A-48686	Sequence 48686, A
29		956	65.2	1418	9	US-10-831-286A-48691	Sequence 48691, A
30		956	65.2	1418	9	US-10-831-286A-48692	Sequence 48692, A
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33	c	944.4	64.4	1436	9	US-10-831-286A-48667	Sequence 48667, A
34		844.6	57.6	1485	14	US-11-055-637-76	Sequence 76, Appl
35		838	57.1	1545	14	US-11-055-637-66	Sequence 66, Appl
36		831.4	56.7	1587	11	US-11-273-617-8	Sequence 8, Appli
37		829.4	56.5	1510	11	US-11-273-617-9	Sequence 9, Appli
38		827	56.4	1521	14	US-11-151-847-1	Sequence 1, Appli
39	c	826.4	56.3	3657	8	US-10-793-626-4187	Sequence 4187, Ap
40		825.6	56.3	1509	11	US-11-273-617-6	Sequence 6, Appli
41		824.2	56.2	1535	14	US-11-055-637-74	Sequence 74, Appl
42		823.2	56.1	1555	5	US-09-941-095-160	Sequence 160, App
43		823.2	56.1	1555	11	US-11-198-746-160	Sequence 160, App
44		823.2	56.1	1555	11	US-11-198-794-160	Sequence 160, App
45		823.2	56.1	1555	11	US-11-198-657-160	Sequence 160, App

ALIGNMENTS

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RESULT 1
US-11-198-242-2
; Sequence 2, Application US/1198242
; Publication No.US20060035345A1
; GENERAL INFORMATION:
;   APPLICANT: AJINOMOTO CO., INC.
;   TITLE OF INVENTION: Process for the production of beta-amino acids by using acylase
;   FILE REFERENCE: AB04037
;   CURRENT APPLICATION NUMBER: US/11/198,242
;   CURRENT FILING DATE: 2005-08-08
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1522
;   TYPE: DNA
;   ORGANISM: Burkholderia sp.
;   FEATURE:
;   NAME/KEY: 16S rDNA
;   LOCATION: (1)..(1522)
;   OTHER INFORMATION:
US-11-198-242-2

Query Match            77.3%;     Score 1133.4;     DB 11;     Length 1522;
Best Local Similarity  88.0%;     Pred. No. 0;
Matches 1294;   Conservative  0;   Mismatches 166;   Indels 11;   Gaps 5;

Qy     1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCAAGCGGCAG 60
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Db     5 TTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCAAGCGGCAG 64

Qy    61 CACGGGTGCTTGCACCTGGTGGCGAGTGGGAGTGGCGGACGGGTGAGTAATGCATCGGAACGGTGTC 120
           |||||||   ||||||||||||     ||||||   ||||||||||||||||| |||||||||||||
Db    65 CGCGGGGGC--AACCCTGCGGCGACGGGTGCGGAACGGGTGAGTAATACATCGGAACGGTGTC 122

Qy   121 CAGAAGTGGGGGATAACCGATCGAAAGATGTGCTAATACCGCATATTCTTACGGAGAA 180
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Db   123 CTGTAGTGGGGGATAGCCCGGCGAAAGCCGGATTAATACCGCATACGCTTCTACGGAGAA 182

Qy   181 AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGGCCGATGCCGATGGCAGATTAGTTAGTTGGT 240
           || |||||||| || ||||||  |||| |||| |||||||||   |||||| |||||||||||||||
Db   183 AGGGGGGGGATCTTAGGACCTTCCGCTACAGAGGGGGGGGCCGATGGGCGAGATTAGTTAGTTGGT 242
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Fri Apr 7 06:40:06 2006

us-10-659-983a-18.rnpbn

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Qy   1318  GGAATCGCTAGTAGTAATCGCGGATCAGCATGCTCGCGGTGAATACGTTCCCGGGTCTTGTGTACA  1377
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Db   1318  GGAATCGCTAGTAGTAATCGCGGATCAGCATGCTCGCGGTGAATACGTTCCCGGGTCTTGTGTACA  1377

Qy   1378  CACCGCCCGTCACACCATGGGAGTGGGTTCACCAGAAGCAGATAGTCTAACCGTAA-GA  1436
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Db   1378  CACCGCCCGTCACACCATGGGAGTGGGTTTACCAGAAGTGGCTAGTCTAACCGCAAGGA  1437

Qy   1437  GGGCGTTTGCCAGGCGAGATTCATGACTGG  1467
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RESULT 2
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; Sequence 1, Application US/11198242
; Publication No. US20060035345A1
; GENERAL INFORMATION:
;   APPLICANT: AJINOMOTO CO., INC.
;   TITLE OF INVENTION: Process for the production of beta-amino acids by using acylase
;   FILE REFERENCE: AB04037
;   CURRENT APPLICATION NUMBER: US/11/198,242
;   CURRENT FILING DATE: 2005-08-08
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1526
;   TYPE: DNA
;   ORGANISM: Variovorax sp.
;   FEATURE:
;   NAME/KEY: 16S rDNA
;   LOCATION: (1)..(1526)
;   OTHER INFORMATION:
US-11-242-1

Query Match             77.2%;  Score 1131.8;  DB 11;  Length 1526;
Best Local Similarity   87.8%;  Pred. No. 0;
Matches 1292; Conservative 0; Mismatches 172; Indels 7; Gaps 5;

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Qy    61  CACGGGTGCTTGCACCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTC  120
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Db    65  CGCGGGAGC--AATCCTGGCGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACGTGCC  122

Qy   121  CAGAAGTGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA  180
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Db   123  CAATCGTGGGGGATAACGCACGCAGCGAAAGCTGTGCTAATACCGCATACGACGATGAA  182

Qy   181  AGCAGGGGATCGAAAGACCTTGTGCTTTCGCGGCGAATGCGCGATTAGCGGGTCAGTTGGT  240
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Db   183  AGCAGGGGATCGCAAGACCTTGCGCGGCGAATGCGCGATTCAGCAGATTAGTTAGTTGGT  242

Qy   241  GGGGTAAAGGCCTACCAAGGCAACAGATCAGTAGTTGGTGAGGTAATGGCTCACCAAGCC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243  GAGGTAAAGGCTCACCAAGGCGACGATCCGTAGCTGGTCTGAGAGGACGACCAGCCACAC  302

Qy   301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  362

Qy   361  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGTTGTAAAGCTC  419
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Qy   420  TTTCAGTCGAGAAAAGGTTGCGTTGAGGATAATCACAACTTATGTACCGACAGAA  479
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Db   423  TTTTGTCAGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGACGGTACCGTAAGAA  482

Qy   480  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  539
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Db   483  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGGGTGCAAGCGTTAATC  542
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Qy   241  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTGCTCGAGAGGACGACCAGCCACAC  300
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Db   243  GGGGTAAAGGCCTACCAAGGCGACGATCTGTAGCTGGTCTGAGAGGACGACCAGCCACAC  302

Qy   301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
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Db   423  TTTCCGGAAAAGAAAAACGGTCCCCGAAAGGGGCGCCGAAAGG  482

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Qy   540  GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCCTTTGTAAGTCAGATGTGAAAATCCCCGG  599
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Qy   600  GCTTAACCTGGGAATTGCGTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAA  659
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Qy   660  TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGGCGAAGGCAGCC  719
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Db   663  TTCCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCC  722

Qy   720  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACC  779
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   723  CCCTGGGCCAATACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACC  782

Qy   780  CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTGAC  839
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   783  CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAAC  842

Qy   840  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  899
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   843  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  902

Qy   900  AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  959
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   903  AATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAA  962

Qy   960  ACCTTACCTACCCTTGACATGTGAGCGAATATTTAGAGATAAAATAGTGCC--TTCGGGA  1017
          |||||||||||||  |  ||||||   ||||| ||||||||||||      ||||||||
Db   963  ACCTTACCTACCCTTGACATGTATGCTGCCTGCCGAGAGGTGGGCTTTCCCGAAAGGGA  1022

Qy   1018  ACGCTAACACAGGTGCTGCAAGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGT  1077
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Qy   1078  CCCGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTTAGTTGGGCACTTAATGAG  1137
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Qy   1138  ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGG  1197
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Db   1138  ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGG  1197

Qy   1198  GTAGGGCTTCACACGTCATACAATGGCCGGTAATACAGAGGGTTGCCAACCCGCGAGGGGGAG  1257
           |||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||
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Qy   1258  CTAATCTCAGAAAGCCGGTCGTAGTCCGGATCCGGATCCGTGCACACTCTGCAACTCGACTCCGTGAAGTC  1317
           ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258  CCAATCCCAGAAAACCGATCGTAGTCCGGATCCGTGCACACTCTGCAACTCGACTCCGTGAAGTC  1317
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;  TITLE OF INVENTION: Novel Microorganisms and Uses Therefor
;  FILE REFERENCE: 11752-006US1
;  CURRENT APPLICATION NUMBER: US/10/515,311
;  CURRENT FILING DATE: 2004-11-22
;  PRIOR APPLICATION NUMBER: PCT/NZ2003/000100
;  PRIOR FILING DATE: 2003-05-22
;  PRIOR APPLICATION NUMBER: NZ 519137
;  PRIOR FILING DATE: 2002-05-22
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 5
;  LENGTH: 1405
;  TYPE: DNA
;  ORGANISM: Acidivorax temperans
US-10-515-311-5

Query Match             72.8%;   Score 1067.6;  DB 9;  Length 1405;
Best Local Similarity   86.8%;   Pred. No. 0;
Matches 1224;  Conservative 0;  Mismatches 174;  Indels 12;  Gaps  4;
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Db    57  ACGGGTGAGTAATACATCGGAACGTGTCCCGATCGTGGGGGATAACGAAGCGAAAGCTTTG  116

Qy   153  CTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGCAAAGACCTTGTGTCTTTTGGA  212
Db   117  CTAATACCGCATACGATCTACGGATGAAAGCAGGGGACCGCAAGGCCTTGCGCGAACGGA  176

Qy   213  GCGGCCGATGCCTGATTAGCTAGTTGGTGTGGTAAAGGCGCTACCAAGGCAACGATGATCAGTA  272
Db   177  GCGGCCGATGCCGGATTAGCTAGTTGGTGGGGTAAAAGCTTACCAAGGCGACGATCTGTA  236

Qy   273  GTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGGCCCAGACTCCTACGGG  332
Db   237  GCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGGCCCAGACTCCTACGGG  296

Qy   333  AGGCAGCAGTGGGGAATTTGACAATGGGCGCAAGCCTGATCCAGCCAATGCCGCGTGAG  392
Db   297  AGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGCA  356

Qy   393  TGAAGAAGGC-TTCGGGTTGTAAAGCTCTTTCAGTCGGGAGAAAAAGGTTGTGACTAATA  451
Db   357  GGATGAAGGCCTTCGGGTTGTAAACTGCTTTTGTACGGAACGAAAAGACTCTGTTAATA  416

Qy   452  ATCACAACTTATGATGTCAGAGGAAGCACCGGCTAACTACGTGCCAGCAGCCGC  511
Db   417  CCTGGGGTCCATGACGGTACTCGAAGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGC  476

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Qy   572  CTTTGTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAATTGCGTTTGTGACTGTAT  631
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Qy   632  AGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAGTGAAATGCGTAGATA  691
Db   597  AGCTAGAGTACCGGCAGAGGGGGATGGAATTCCCGCGTGTAGCAGTGAAATGCGTAGATATG  656

Qy   692  TGGAAGAACATGCGATGGCGAAGGCAGCCCCCTGGGTTAACACTGACGCTCATGCACGAAA  751
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Qy   752  GGCTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTA  811
Db   717  GCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTG  776

Qy   812  GTTGTTTGGGCCTTACTAGGCTTGGTTGGTAACGTAGCTAGCTAACGCGTGAAGTTGACCGCTGGGGGA  871
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Db   483  TAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  542

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Db   543  GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTGAATTGTAAGACAGTTGTGAAATCCCCGG  602

Qy   600  GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTAGCAGAGGGGGGTGGAA  659
Db   603  GCTCAACCTGGGAACTGCCATCGTGACTGCTGAGACTCGAGTACGGCAGAGGGGGATGGAA  662

Qy   660  TTCCATGTGTAGCAGTGAAATGCGTAGATATGCGGAGGAACATGGCAAGGCAGCC  719
Db   663  TTCCGCGTGTAGCAGTGAAATGCGTAGATATGCGGAGGAACACCGATGGCGAAGGCAATC  722

Qy   720  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC  779
Db   723  CCCTGGGCCTGTACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC  782

Qy   780  CTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGTCTTCACTGACTCAGTCAGTAAC  839
Db   783  CTGGTAGTCCACGCCGTAAACGATGTCAACTGGTTGTTGGGTCTTCACTGACTCAGTAAC  842

Qy   840  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGG  899
Db   843  GAAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGG  902

Qy   900  AATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGTTTAATTCGATGCAACGCGAAAA  959
Db   903  AATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGTTTAATTCGATGCAACGCGAAAA  962

Qy   960  ACCTTACCTGCCTTTGACATGTAGCGAATATTTTAGAGATAAAATAGTG--CCTTCGGGA  1017
Db   963  ACCTTACCCACCTTTGACATGTACGGAATGTTGCCAGAGATGGCTTAGTGCTCGAAAGAGA  1022

Qy  1018  ACGCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGT  1077
Db  1023  ACGGTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGT  1082

Qy  1078  CCCGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGCACTTAATGAG  1137
Db  1083  CCCGCAACGAGCGCAACCCTTGTCATTAGTTGCTA-CATTCAGTTGGGCACTCTAATGAG  1141

Qy  1138  ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGG  1197
Db  1142  ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATAG  1201

Qy  1198  GTAGGGCTTCACACGGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAG  1257
Db  1202  GTGGGGCTACACACGTGCTACAACAATGGCGGGTACAAAGGGTTGCCAACCCGCGAGGGGGAG  1261

Qy  1258  CTAATCTCAGAAAGCCGGTCTCAGTTCGGATCCGGAGTCTGCAACTCGACTCCGTGAAGTC  1317
Db  1262  CTAATCCCATAAAAACCAGTCGTAGTCCGGATCCGCAGTCTGCAACTCGACTGCGTGAAGTC  1321

Qy  1318  GGAATCGCTAGTAATCGCGGATCAACATGTCGCGGTGAATACGTTCCCGGGTCTTGTACA  1377
Db  1322  GGAATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACA  1381

Qy  1378  CACCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGTAGCTAGTCTAACCGTAA-GA  1436
Db  1382  CACCGCCCGTCACACCATGGGAGCGGGTTCTGCCAGAAGTAGTTAGCTTAACCGCAAGGA  1441

Qy  1437  GGGCGTTTGCCACGGCAGATTCATGACTGG  1467
Db  1442  GGGCGATTACCACGGCAGGGTTCGTGACTGG  1472
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US-10-513-639-1

Query Match       69.4%;   Score 1018.8;  DB 9;   Length 1501;
Best Local Similarity  83.4%;   Pred. No. 6.6e-304;
Matches 1228;  Conservative    0;  Mismatches 237;  Indels    7;  Gaps    6;

Qy      1  TTGATCATGGCTCAGATTGAACGCTGGCCGCATGCTTCTTACATGCAAGTCGAACGCGCAG   60
           ||||||||||||||||||||||||||||||| |||||||||| |||||||||||||||
Db      6  TTGATCATGGCTCAGATTGAACGCTGGCCGCAGGCCTAACACATGCAAGTCGAGCGG-AT   64

Qy     61  CACGGGTGCTTGCACCTGCTGGCGAGTGGCGACGGGTGAGTAATGCATCGGAACGTGTC  120
           ||||||||| |||||||      ||||||||||||||||||| |||||||| |||||
Db     65  GAGAAGAGCTTGCTCTTCGATTC-AGCGGCGGACGGGTGAGTAATGCCTAGGAATCGCC  123

Qy    121  CAGAAGTGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTTACGGAGGAA  180
           |||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    124  TGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTAATACCGCTAATACCGTCCTACGGGAGAA  183

Qy    181  AGCAGGGGATCGAAAGACCTTGTCTTGTGCCGGCGCCGATGCCTGATTAGCTAGTTGGT  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184  AGCAGGGGACCTTCGGGCCTTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGT  243

Qy    241  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  300
           ||||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||
Db    244  GAGGTAATGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACAC  303

Qy    301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304  TGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATG  363

Qy    361  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAGG--CTTCGGGTTGTAAAGCTC  419
           |||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db    364  GGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCAC  423

Qy    420  TTTCAGTCGAGAAGAAAGGTTGTGACTAATAATCACAACGTTGTTTTGACGTTACCGACAGAA  479
           ||| |||||||||||| |||||||||||||||||||||| ||||||  ||||||||||||||
Db    424  TTTAAGTTGGGAGGAAGGGCATTAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAA  483

Qy    480  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  539
           ||||||||||||||||| |||||||||||||||||||||||||||| |||||||||||||
Db    484  TAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATC  543

Qy    540  GGAATTACTGGGCGTAAAGCGCGCGTAGGCGGTTGGTTGTTAAGTTGGATGTGAAATCCCGG  599
           |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    544  GGAATTACTGGGCGTAAAGCGCGCGTAGGCGGTTTGTTAAGTCGCAGATGTGAAAGCCCCGG  603

Qy    600  GCTTAACCTGGGAATTGCGTTGAAAACTACAAAGCTAGAGTGTAGCAGAGGGGTGGTCGAA  659
           |||||||||||||||||||||  |||||||||||||| |||||| ||||| |||||||||
Db    604  GCTCAACCTGGGAACTGCGTATCCAAAACTGGCAAGCTAGAGTACGGTAGAGGGTGGTGGAA  663

Qy    660  TTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCC  719
           ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    664  TTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACC  723

Qy    720  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC  779
           |||||||||||||| ||||| ||||||||||||||||||||| |||||||||||||||||
Db    724  ACCTGGACTGATACTCTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC  783

Qy    780  CTGGTAGTCCACGCCCTAAACGATGTCAACTAGCTGTTGG-GCCTTACTAGGCTTGGTAA  838
           |||||||||||||||||||||||||| |||||||| |||| ||||||||||| |||||||
Db    784  CTGGTAGTCCAACGCCGTAAACGATGTCAACTAGCCGTTGGGAGCCTTGAGATTTTAGTGG  843

Qy    839  CGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAG  898
           || |||||||||||||||||||| ||||||||||||||| |||||||||||||||||||||
Db    844  CGCAGCTAACGCATTAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAT  903

Qy    899  GAATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGTTTAATTCGAAGCAACGCGAAG  958
           ||||||||||||| |||||||||||||||||| |||| ||||||||||||||||||||||
Db    904  GAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAG  963

Qy    959  AACCTTACCTACCCTTGACATGCATGCCTTGACATGGGGGAATATTTAGAGATAAAATATGTGC  1018
           ||||||||||||||||||||||| ||||||||||||||||| || ||||| || |||||||
Db    964  AACCTTACCAGCCTTGACATGCATGCAGAGACTTTCCAGAGATGGATTGGTGCCTTCGGGAA  1023
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Db    777  GTTGGTGGGTCTTCACTGACTAGCAGAAGCTAACGAGCCGTGAGGTTGACCGGCCTGGGGA  836
           ||||||||| |||  ||  ||||||||||||||||||||||||||||||||||||||||
Qy    872  GTACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTA  931

Db    837  GTACGGCCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATGA  896

Qy    932  TGTGGATTAATTCGATGCAACGCGAAGAAACCTTACCTACCCTTGACATGTAGCGGAATATT  991
           || ||||||||||||| |||||||| |||||||||| |||  |||||||||||||||| ||
Db    897  TGTGGTTTAATTCGATGCAACGCGAAGAAACCTTACCCACCTTTGACATGTACGGAATCCT  956

Qy    992  TTAGAGATAAATAGTG--CCTTCGGGAACGCTAACACAGGTGCTGCATGGCTGTCGTCA  1049
           |||||||||||||  |  |||||| ||||||||||||||||||||||||||||||||||
Db    957  TTAGAGATAGGAGGAGTGCTCGAAAGAGAGACACAGGTGCTGCATGGCTGTCGTCA  1016

Qy   1050  GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCATTAATTG  1109
           ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   1017  GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGCCATTAGTTG  1076

Qy   1110  CCATCATTTAGTTGGGCACTTTAATGACTGCCGGTGACAAACCGGAGGAAGGTGGGGA  1169
           || ||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1077  CTACGA-----AAGGGCACTCTAATGGGACTGCCGGTGACAAACCGGAGGAAGGTGGGGA  1131

Qy   1170  TGACGTCAAGTCCTCATGGCCCTTATGGGTTAGGGGCTTCACACGTAATACAAATGGCGCGTA  1229
           ||||||||||||||||||||| ||||| ||||| |||||||||||| |||||| ||||||||
Db   1132  TGACGTCAAGTCCTCATGGCCCTTATAGGTGGGGCTACACGTCATACACGTGCTGGTA  1191

Qy   1230  CAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGGCGTCGTAGTCCGGATC  1289
           ||||||||||||||||||||||||| ||||||||  |||||||||||||||||||||||||
Db   1192  CAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCCCATAAAGCCAGTCGTAGTCCGGATC  1251

Qy   1290  GGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCGCGGATCAGCATGCCG  1349
           || ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1252  GCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGGATCAGAATGTCG  1311

Qy   1350  CGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACATGGGAGTGGGTTTCA  1409
           |||||||||||||||||||||||||||||||||||||||||||||| |||| |||||
Db   1312  CGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGCGGGTTCTG  1371

Qy   1410  CCAGAAGCAGATAGTCTAACCGTAAGGAGG  1439
           |||||||| ||||||||||||||||||||
Db   1372  CCAGAAGTAGGTAGCCTAACCGTAAGGAGG  1401
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RESULT 4
US-10-513-639-1

; Sequence 1, Application US/10513639
; Publication No. US20060010511A1
GENERAL INFORMATION:
;  APPLICANT:  Sun, Yicheng
;  APPLICANT:  Chen, Yancheng
;  APPLICANT:  Li, Pengmei
;  APPLICANT:  Tian, Zhexian
;  APPLICANT:  Lin, Min
;  APPLICANT:  Wang, Yiping
;  TITLE OF INVENTION:  NOVEL GLYPHOSATE-TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE AND THE GENE
;  TITLE OF INVENTION:  ENCODING THE SAME
;  FILE REFERENCE:  18495-002US1
;  CURRENT APPLICATION NUMBER:  US/10/513,639
;  CURRENT FILING DATE:  2004-11-05
;  PRIOR APPLICATION NUMBER:  CN 02117991.3
;  PRIOR FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER:  CN 02117647.7
;  PRIOR FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER:  PCT/CN02/00539
;  PRIOR FILING DATE:  2002-08-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 1501
;  TYPE: DNA
;  ORGANISM: Pseudomonas putida P.P4G-1
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Qy   182  GCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGGCCGATGCCTGATGATTAGCTAGTTGGTG  241
          ||||||||||  ||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   181  GCAGGGGACCTTCGGGCCTTGCCGTGTCCGATGAACCCATATGGGATTAGCTAGTAGGTG    240

Qy   242  GGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACT  301
          |||||| |||||||||||||||||||||||  |||  |||||||||||||||||||||||
Db   241  AGGTAATGGCTCACCTAGGCGACGATCTCTAGTCACCAGCACGTAATGGTGGGCACTCAAGGA  300

Qy   302  GGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGG  361
          |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db   301  GGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATCG    360

Qy   362  GCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCT  420
          ||| ||||||||||||||||||||||||||||||||||||  |||||||||||||||||| 
Db   361  GCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTAGGGTTGTAAAGTACT   420

Qy   421  TTCAGTCGAGAGAAAAGGTTGTGACTAATAATCACAACTTATGATGTGACCAGAGAAG    480
          |||||||  |||||||||||||||| ||||||||||||||||||| |||||||||||||
Db   421  TTCAGTCGGGAGGAAGGGCGTTAATCTAATACTAATATCAGCGATGACGTTACCGACAGAAG  480

Qy   481  AAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGGGGGTGCAAGCGTTAATCG    540

Qy   541  GAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGG  600
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   541  GAATTACTGGGCGTAAAGCGCACGCAGGCGGTGATTAGTGTAAGTGTGAAATCCCCGGG    600

Qy   601  CTTAACCTGGGAATTGCGTTTGGCATCCAAAATGCTAGAGATATGGAAGACATCGATGGCC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  CTTAACCTGGGAATTGCATCTAAAACTGGTCAGCTAGAGTCTTGTAGAGGGGGTAGAAT    660

Qy   661  TCCATGTGTAGCAGTGAAATGCGTAGAGATATGAAGAACATCGATGGCGAAGGCAGCCC  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  TCCATGTGTAGCGGTGAAATGCGTAGAGATGTGGGAGGAATACCGGTGGCGAAGGCGGCCCC  720

Qy   721  CCTGGGTTAACACTGACGCTCAGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCC  780
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  CCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCC  780

Qy   781  TGGTAGTCCACGCCGTAAACGATGTC-AACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC  839
          |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db   781  TGGTAGTCCACGCCGTAAACGATGTCGATTTGGAGGTTGTTCCCTTGAGGAGTGGCTTCC   840

Qy   840  GTAGCTAACGGTGAAGTTGACCGCCTGGGGAGTACGTCGCAAGATTAAAACTCAAAGG  899
          | ||||||| ||||| ||||||  ||||||||||||||||||||||||||||| |||||
Db   841  GGAGCTAACGGTGGTTAAATCGACCGCCTGGGGAGTACGACCGCAAGGTTAAAACTCAAATG  900

Qy   900  AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAA  959
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   901  AATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGA   960

Qy   960  ACCTTACCTACCCTTGACATGCTAGCGAATATTTAGAGATAAAAATAGTGCCTTCGGGAAC  1019
          |||||||||||||||||||||||||||| |||||||| |||||||||||||||||||||||
Db   961  ACCTTACCTACTCTTGACATCCAGAGAATTTAGTGCCTTCGGGAAC    1020

Qy  1020  GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1079
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  TCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCC  1080

Qy  1080  CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTTA--GTTGGGCACTTTAATGAG  1137
          ||||||||||||||||||||  |||||||||||||||||||  ||||||||||||||||||
Db  1081  CGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCACGTAATGGTGGGAACTCAAGGGAG  1140

Qy  1138  ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGG  1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  1141  ACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGA  1200

Qy  1198  GTAGGGCTTCACGTAATACAATGGCGCGTACAAGGGTTGCCAACCCGCGAGGGGAG  1257
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||| 
Db  1201  GTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGAACTCGCGAGAGCAAG  1260
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Qy  1019  CGCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTC  1078
          ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1024  CTTGACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAGATGTTGGGTTAAGTC  1083

Qy  1079  CCGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTTA--GTTGGGCACTTTAATGA  1136
          |||||||||||||||||||||||  |||||||||||||||||  |||||||||||||||||
Db  1084  CCGTAACGAGCGCAACCCTTGTCCTTAGTTGCCAGCACGTAATGGTGGGCACTCTAAGGA  1143

Qy  1137  GACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTATG  1196
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  1144  GACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGGCGTCAAGTCATCATGGCCCTTACG  1203

Qy  1197  GGTAGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGA  1256
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||| 
Db  1204  GCCTGGGCTACACACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGA  1263

Qy  1257  GCTAATCTCAGAAAGCCGCGTCGTAGTCCGGATCGCAGTCTGCAACTCCGTCCGTGAAGT  1316
          |||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1264  GCTAATCTCACAAAACCGATCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGT  1323

Qy  1317  CGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTAC  1376
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1324  CGGAATCGCTAGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTAC  1383

Qy  1377  ACACCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGT-AAG  1435
          |||||||||||||||||||||||||||||||  ||||||||||||||||||||| |||
Db  1384  ACACCGCCCGTCACACCATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGG  1443

Qy  1436  AGGGGCGTTTGCCACGGCGAGATTCATGACTGG  1467
          ||||||||||||||||||||||||||||||||||
Db  1444  AGGACGGTTACCACGGTGTGATTCATGACTGG  1475
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RESULT 5

US-10-831-286A-48682

; Sequence 48682, Application US/10831286A
; Publication No. US2006004246A1
GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 02796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48682
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: Moellerella wisconsensis

US-10-831-286A-48682

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Query Match         68.8%;  Score 1009; DB 9; Length 1510;
Best Local Similarity 83.1%;  Pred. No. 7.1e-301;
Matches 1222; Conservative 0; Mismatches 240; Indels 9; Gaps 6;

Qy    6  CATGGGTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACG-  64
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  CATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAACGGTAACAGGA  60

Qy   65  -GGTGCTTGCACC--TGGTGGCGAGTGGCGAACGGGTGAGTAATGTCATCGGAACGTGTCC  121
         | |||||||| ||   ||||||||||||||||||||||||||||||||||||||||||||
Db   61  AGGAGCTTGCTCTTCTTGCTGACGAGCGGCGGACGGGTGAGTAATGTATGGGATCTGCCT  120

Qy  122  AGAAGTGGGGATAACCGATCGGAAAGATGTGCTAATACCGCATATTCTTCTACGGAGGAAA  181
         ||||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  121  GACAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAG  180
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RESULT 6
US-10-831-286A-48680
; Sequence 48680, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48680
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: Moellerella wisconsensis
US-10-831-286A-48680

Query Match   68.7%;   Score 1007.4;   DB 9; Length 1510;
Best Local Similarity 83.0%;   Pred. No. 2.2e-300;
Matches 1221; Conservative   0; Mismatches 241; Indels   9;   Gaps   6;

Qy   6 CATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAGCACG-   64
            ||||||||||||||||||| ||||||||||| |||| ||||||||||||| ||| |||
Db   1 CATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAACAGGA   60

Qy   65 -GGTGCTTGCACC--TGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCC 121
            |||| |||| || ||| ||||| ||| || |||||||||||||| ||| ||||
Db   61 AGAAGCTTGCTTCTTTGCTGACGAGCGGCGGACGGGTGAGTAATGTATGGGGATCTGCCT 120

Qy   122 AGAAGTGGGGGATAACCGATCGAAAGATGTGCTAATACCGGATATTCTCTACGGAGGAAA 181
            |||||||||||||||| || | || ||||||| ||||||| ||| |||||||||||||||
Db   121 GACAGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAATCTCTTAAGAGGAAA 180

Qy   182 GCAGGGGATCGAAAGACCTTGCTGTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTG 241
            |||||||||| |||| | || ||||||||||||| |||||||||| ||||||||||||
Db   181 GCAGGGGACCTTCGGGCCTTGCGCTATCGGATGAACCCATATGGGATTAGCTAGTAGGTG 240

Qy   242 GGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACT 301
            |||||||||||| ||||||| ||| ||| ||||||||||||||| |||||||| |||||
Db   241 GGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACT 300

Qy   302 GGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGG 361
            ||||||||||||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db   301 GGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGG 360

Qy   362 GCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCT 420
            ||||||||| ||||||||||||| | ||| |||||||||| ||||||||||||||| ||
Db   361 GCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTAGGGTTGTAAAGTACT 420

Qy   421 TTCAGTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACGAGTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   421 TTCAGTCGGGAGGAAGGCGTTGATTAATAATCATCAGCGATTGACGTTACCGACGAGAAG 480

Qy   481 AAGCACCGGCTAACTCGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCG 540
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   481 AAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGGGGTGCAAGCGTTAATCG 540

Qy   541 GAATTACTGGGCGTAAAGGGTGCGCAGGCGGCCGTTTGTAAGTCAGATGTGAAATCCCCGGG 600
            |||||||||||| ||||| ||| ||||||| || ||| | ||||||| ||||||||||||||
Db   541 GAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCGGG 600

Qy   601 CTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTGAGAGAGGGGGGTGGAAT 660
            || ||||| |||| | || || |||||||||||||||||| | ||||||||||||||
Db   601 CTCAACCTGGGAATGGCATCTAAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAAT 660

Qy   661 TCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACACGATGGCGAAGGCAGCGCCC 720
            |||| ||||| ||||||||| |||||| || ||| ||||| ||||||||||||| |||||
Db   661 TCCATGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCC 720

Qy   721 CCTGGGTTAACACTGACGCTCATGCGAAAGCGTGGGGAGCAAACGGTTAGATAGATACCC 780
            |||||||||| ||| |||| ||||||||| ||||||||||| |||| |||||||||||||
Db   721 CCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCC 780

Qy   781 TGGTAGTCCACGCCCTAAACGATGTC-AACTAGTTGTTGGGCTTACTAGGCTTGGTAAC 839
            ||||||||| ||||| |||||||||| |||||| |||||||| |||||| |||||||||
Db   781 TGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGGTTGTTCCCTTGAGGAGTGGCTTCC 840

Qy   840 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG 899
            ||||||||| |||||||||| || ||||||||||| |||| ||| || ||||||||||
Db   841 GGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATG 900

Qy   900 AATTGACGGGGACCCCACAAGCGGTGGATTATGTGGCTTAATTCGATGCAACGCGAAAA 959
            |||||||||||| ||||||||||||||||||| ||| ||||||||||||||||||||||
Db   901 AATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGA 960

Qy   960 ACCTTACCTACCCTTGACATGCCAGGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1019
            |||||||||||||||||||||| | |||||||| ||||||||||| ||| || |||||||
Db   961 ACCTTACCTACTCTTGACATCCAGAGAATTTTGCAGAGATGCTTTAGTGCCTTCGGGAAC 1020

Qy   1020 GCTAACACAGGTGCTGCAACCCTTGTCGTCTCAGCTCGTCGTGAGATGTTGGGTTAAGTCC 1079
            ||||| |||||||| |||| |||||| | | |||||||||||| ||| ||| ||||| |
Db   1021 TCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCC 1080

Qy   1080 CGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTTA--GTTGGGCACTTTAATGAC 1137
            ||||||||||||||| ||||||| | |||||||||||| | |||||||| |||||
Db   1081 CGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCACGTAATGGTGGGCACTCTAAGGAG 1140

Qy   1138 ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTATGG 1197
            |||||||| |||||||| || |||||||||||| |||||||| |||||| ||||| ||||
Db   1141 ACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGA 1200

Qy   1198 GTAGGGCTTCACATGCTACAATGGCGCGTACAAAGGGTTGCCAACCCGCGAGGGGGAG 1257
            |||||| ||||| |||| ||||||||| || || |||||||||||| || |||| ||||
Db   1201 GTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGAACTCGCGAGAGCCAG 1260

Qy   1258 CTAATCTCAGAAAGCGCGTCTCAGTCGGATCGGCTGCGACTCCGTGAGTC 1317
            | ||||| ||||| |||||||| ||||||| ||| ||||||||||||| |
Db   1261 CGGAACTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTC 1320

Qy   1318 GGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACA 1377
            |||||||||||||||||| |||| ||| | ||||||||| ||||||||||||||||||||
Db   1321 GGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCGGGTCTTGTACA 1380

Qy   1378 CACCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGTCTAACCGT-AAGA 1436
            |||||||||||||||||| |||||||||||||| ||||| | ||||| |||
Db   1381 CACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGTAGCTTAACCTTCGGGG 1440

Qy   1437 GGGCGTTGCCACGGCGAGATTCATGACTGG 1467
            |||| ||| || |||||||||| |||||||
Db   1441 GGGCGTTACCACTTTGTGATTCATGACTGG 1471

RESULT 7
US-10-831-286A-48684
; Sequence 48684, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48684
; LENGTH: 1508
; TYPE: DNA
; ORGANISM: Providencia rustigianii
US-10-831-286A-48684

Query Match   68.6%; Score 1006.6; DB 9; Length 1508;
Best Local Similarity 82.6%; Pred. No. 3.9e-300;
Matches 1213; Conservative 0; Mismatches 249; Indels 7; Gaps 5;

Qy   6 CATGGGTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAGCACGG   65
            |||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Db   1 CATGGGTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAACAGGG   60

Qy   66 G--TGCTTGCACCTGGTGGCGAGTCGCGGCGGGTGAGTAATGCATCGGAACGGTGTCCAG 123
            | |||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||
Db   61 GAAGCTTGCTTCTCGCTGACGAGCGGCGGACGGGTGAGTAATGTATGGGATCTGCCCGA 120

Qy   124 AAGTGGGGGATAACGCATCGAAAGATGTCTAATACCGCATATTCTCTACGGAGGAAAGC 183
            |||||||||||||||||||||||| |||| ||||||||||||| |||||||| ||||||
Db   121 TAGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAATCTCTTTGGAGCAAAGC 180

Qy   184 AGGGGATCGAAAGACCTTGTCGCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGG 243
            |||||| || ||||||||||||||||||| ||||||||||||||||||||||||||||
Db   181 AGGGGGAACTTCGGTCCTTGGCGCTATCGGATGAACCCATATGGGATTAGCTAGTTGGTGGG 240

Qy   244 GTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGG 303
            |||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   241 GTAATGGCTCACCAAGGCGACGATCCCTAGCTGGTCTGAGAGGATGATCAGCCACACTGG 300

Qy   304 GACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGC 363
            ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   301 GACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGC 360

Qy   364 GAAAGCCTGATCCAGCAAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTT 422
            ||||| |||||||||||| |||||||||| |||||||||| ||||||||||||||||| ||
Db   361 GCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTAGGGTTGTAAAGTACTTT 420

Qy   423 CAGTCGGAGGAAGAAAAGGTTGTGACTAATAATCACAACTTATGATGTGTACCAGCAGAAGAAGAA 482
            |||||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||
Db   421 CAGTTGGGAGGAAGGGCGTTGATGCTAATATCATCAGCGATTGACGTTACCAACAGAAGAA 480

Qy   483 GCACCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGA 542
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGA 540

Qy   543 ATTACTGGGCGTAAAGCGTGCGCAGGCGGCCGGTTGAAGTCAGATGTGAAATCCCCGGGCT 602
            ||||||||||||||||||| ||| |||||||||||||| ||||||||||||||||||||||||
Db   541 ATTACTGGGCGTAAAGCGCACGCAGGCGGTTTGTTAAGTTAGATGTGAAATCCCCGGGCT 600

Qy   603 TAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTC 662
            |||| |||||||| ||||||| |||| |||||||||||||| ||||||| ||||||||||||
Db   601 TAACCTGGGAATTGCATCTGATACTGGCAAGCTTGAGTCTCGTAGAGGGGGGTAGAATTC 660

Qy   663 CATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCC 722

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;  SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 48685
;  LENGTH: 1508
;  TYPE: DNA
;  ORGANISM: Providencia rustigianii
US-10-831-286A-48685

Query Match       68.6%;   Score 1006.6; DB 9; Length 1508;
Best Local Similarity 82.6%;   Pred. No. 3.9e-300;
Matches 1213; Conservative 0; Mismatches 249; Indels 7; Gaps 5;

Qy      6 CATGGCTCAGATTGAACGCTGGCGGCGCATGCTTACACATGCAAGTCGAACGGCAGCACGG 65
            ||||||||||||||||||||||||| |||| |||||||||||||||||| ||| ||| ||
Db      1 CATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAACAGGA 60

Qy     66 G--TGCTTGCACCTGGTGGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAG 123
            |  |||||||||||||||   |||||||||||||||||||||||||||| | |||||||||
Db     61 GAAGCTTGCTTCTCGCTGACGAGCGGCGGACGGGTGAGTAATGTATGGGGATCTGCCCGA 120

Qy    124 AAGTGGGGGATAACCGATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGC 183
            ||||||||| ||  ||||||||||   ||| ||||||||||| || ||||| ||||||||
Db    121 TAGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAATCTCTACGGAGCAAAGC 180

Qy    184 AGGGGATCGAAAGACCTTGTCTTTTGGAGCGGCCGATGCGTGATTAGCTAGTTGGTGTGGG 243
            ||||||   |||  | |||||||||| || |||| ||||| ||||||||||||||||||||
Db    181 AGGGGAACTTCGGTCCTTGCGCTATCGGATGAACCCATATGGGATTAGCTAGTAGGTGTGGG 240

Qy    244 GTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGG 303
            ||||| |||||| |||||| || |||  |||||| ||||||||||| |||||||||||||
Db    241 GTAATGGCTCACCTAAGGCGACGATCCCTAGCTGGTCTGAGAGGATGATCAGCCACACTGG 300

Qy    304 GACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGC 363
            |||||||||| |||||||||||||||||||||||||||||||||||| | || |||||||
Db    301 GACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGC 360

Qy    364 GAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG--CTTCGGGTTGTAAAGTCTTT 422
            ||||||||| || |||||||||||||||||| |||| |  ||||||| |||||||| || |
Db    361 GCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTAGGGTTGTAAAGTACTTT 420

Qy    423 CAGTCGAGAGAAAAGGTTGTGACTAATAATAATCACAACTTATGATGTGTACCGACAGAGA 482
            ||||||||||||||| ||| |  |||  |||||| |||||||||||||||  ||||||||
Db    421 CAGTTGGGAGGAAGGGGTTAAAGCTAATATCTGTTAACGATTGACGTTACCCAACAGAAGA 480

Qy    483 GCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGA 542
            ||||||||||||||| | |||||||||||||||||| |||||||||||||||||||||||
Db    481 GCACCGGCTAACTACCTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGA 540

Qy    543 ATTACTGGGCGTAAAGGGTGCGCAGGCGGCCTTGTAAGTCAGATGTGAAATCCCCGGGCT 602
            |||||| ||| ||||| | |||||||||||  |||||||||||||||||| |||||||||
Db    541 ATTACTCGGGCGTAAAGGGTGCGTAGGCGGTTGATTAAGTCAGATGTGAAATCCCCGGGCT 600

Qy    603 TAACCTGGGAATTGCGGTTTGAAACTACAAGCTAGAGTGTGAGAGGGGGTGGAATTC 662
            |||| |||||||||   |||||||||||| |||||||| ||| || || | ||||||
Db    601 TAACCTGGGAATTGCATCCTTGAAACTGGTCAGCTAGAGTCTGTAGAGGGGGGTAGAATTC 660

Qy    663 CATGTGTAGCAGTGAAATGCGTAGAGATGCGGAGGAACATCGGTGGCGAAGGCGGCCCCC 722
            |||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||
Db    661 CATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACCGGTGGCGAAGGCGGCCCCCC 720

Qy    723 TGGGGTTAACACTGTCATGCACGAAAGCGTGGGGAGCAAACACGGATTAGATACCCTG 782
            |||| | |  ||||||||||||||| ||||||||||||||| ||||||||||||||||
Db    721 TGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTG 780

Qy    783 GTAGTCCACGCCGTAAACGATGTC-AACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGT 841
            |||||||||||||||||||||||| | |||||| || ||||| || ||||||||| | ||
Db    781 GTAGTCCACGCCGTAAACGATGTCGATTTGGAGGTTGTTCCCTTGAGGAGTGGCTTCCGG 840

Qy    842 AGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAAGGAA 901
            ||||||||||  |||  || ||||  |||||||| |||||||||  ||||| || |||||
Db    841 AGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAA 900

Qy    902 TTGACGGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAAAC 961
            |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    901 TTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAAC 960
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Qy    962 CTTACCTACCCTTGACATGCAGTAGCGATATTTAGAGATAAAATAGTGCCTTCGGGAACGC 1021
            | ||||||||  |||||||||||| ||||| |||||||||||||||||| |||||||||||
Db    961 CTTACCTACTTTGACATCCAGAGAATTAGCAGAGATGCTTTAGTGCCTTCGGGAACTC 1020

Qy   1022 TAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCG 1081
            | | |||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   1021 TGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCG 1080

Qy   1082 CAACGAGCGCAACCCTTGTCATTAATTGCCATCA--TTTAGTTGGGCACTTTAATGAGAC 1139
            |||||||||||||||| ||| |||||| ||| | |  ||| |||||| |||| || ||||
Db   1081 CAACGAGCGCAACCCTTATCCTTTGTTGCCAGCACGTAGGGGAACTCAAAGGAGACT 1139

Qy   1140 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT 1199
            ||||||||| |||||||||||||||||| ||||||||||||||| |||||||||| ||||
Db   1141 TGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGT 1200

Qy   1200 AGGGCTTCACGTGCTACAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1259
            ||||||| ||  | |||||||||| |||||| |||||||| ||| ||| | |||||||||
Db   1201 AGGGCTACACGTGCTACAATGGCGTATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGG 1260

Qy   1260 AATCTCAGAAAGCGCGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGG 1319
            |||| ||| |||| |  || || |||| ||||| ||||||||||||||| ||  ||||||
Db   1261 GAACTCATAAAGTACGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGG 1320

Qy   1320 AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACA 1379
            ||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||||
Db   1321 AATCGCTAGTAATCGTGAATCAGAATGTCACGGTGAATACGTTCCCGGGCCTTGTACACA 1380

Qy   1380 CCGCCCGTCACACCATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCGT-AAGAGG 1438
            ||||||||||||||||||||||||||||||| ||||| |||| ||||||| || |||||
Db   1381 CCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGTTTAACCTTCGGGAGG 1440

Qy   1439 GCGTTTGCCACGGCGGAGATTCATGACTGG 1467
            ||||| || ||| |||||||| |||||||||
Db   1441 GCGCTTACCACTTTGTGATTCATGACTGG 1469
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RESULT 9
US-10-831-286A-48677
;  Sequence 48677, Application US/10831286A
;  Publication No. US2006046246A1
;  GENERAL INFORMATION:
;   APPLICANT: ZENG, QIANDONG
;   APPLICANT: CHATELLIER, SONIA
;   APPLICANT: MOIR, DONALD T.
;   APPLICANT: LACROIX, BRUNA
;   APPLICANT: CHILDRESS, DARRELL
;   TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
;   FILE REFERENCE: 032796-174.001
;   CURRENT APPLICATION NUMBER: US/10/831,286A
;   CURRENT FILING DATE: 2004-04-26
;   PRIOR APPLICATION NUMBER: 60/464,955
;   PRIOR FILING DATE: 2003-04-24
;   NUMBER OF SEQ ID NOS: 48788
;   SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 48677
;  LENGTH: 1507
;  TYPE: DNA
;  ORGANISM: Providencia rettgeri
US-10-831-286A-48677

Query Match       68.6%;   Score 1006; DB 9; Length 1507;
Best Local Similarity 82.6%;   Pred. No. 6e-300;
Matches 1212; Conservative 0; Mismatches 250; Indels 6; Gaps 5;

Qy      6 CATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAGCACGG 65
            |||||||||||||||||||||||||  |||| |||||||||||||||||| ||| ||| ||
Db      1 CATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAACAGGG 60

Qy     66 G--TGCTTGCACCTGGTGGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAG 123
            |  ||||||||||||   ||||||||||||||||||||||||||||| |||||||||||||
Db     66 GGTTGCTTGCACCTGGTGGGCGAGTGGCGGACGGGTGAGTAATGTATCGGAACGTGTCCAG 123
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Db

Qy      61 GAAGCTTGCTTCTCGCTGACGAGCGGCGACGGGTGAGTAATGTATGGGGATCTGCCCGA 120

Qy     124 AAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGC 183
           ||||| |||||||||||| ||||||| ||  ||||||||||||||||||| |||||||||
Db     121 TAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAATCTCTAAGGAGCAAAGC 180

Qy     184 AGGGGATCGAAAGACCTTGTGCTTCGGGCGGCCGATGCCGTAGTTAGTTGGTGGG 243
           ||||||||| ||||||||||||| |||||||||||||||  |||||||||||||||
Db     181 AGGGGAACTTCGGTCCTTGCGCTATCGGATGAACCCCATATGGTCTAGTAGTTGAG 240

Qy     244 GTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGG 303
           |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db     241 GTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGATCAGCCACACTGG 300

Qy     304 GACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGC 363
           ||||||||||||||||||||| ||||||||||||||||||||||||||| |||||||||
Db     301 GACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGC 360

Qy     364 GAAAGCCTGATCAGCAAGAAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAGAA 422
           ||||||| |||||||||||| ||| ||||  ||||  |||||| |||||||| ||||||||||||
Db     361 GCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTT 420

Qy     423 CAGTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAGAA 482
           |||||||||||||||||| ||||||||||||||||| |||||||||||||||||||||
Db     421 CAGTCGGGAGGAAGGGCGGTGATGTCTAATATCATTCATCAACATTTGACGTTACCGACAGAGAA 480

Qy     483 GCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATAACGGCTAGGCGTTGAAGCGTTAATCGGA 542
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGA 540

Qy     543 ATTACTGGGCGTAAAGCGCACGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCCCGGGCT 602
           ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db     541 ATTACTGGGCGTAAAGCGCACGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCCCGGGCT 600

Qy     603 TAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTTCAGAGGGGGGTAGAATTC 662
           ||||||||||| ||||| ||| ||||||||  ||||||||| ||||||| |||||||||
Db     601 TAACCTGGGAATGGCATCTAAGACTGGTCAGCTAGAGTCTTGTAGAGGGGGGTAGAATTC 660

Qy     663 CATGTGTAGCAGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCC 722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACCGGTGGCGAAGGCGGCCCCC 720

Qy     723 TGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACCCTG 782
           |||| ||||||||||||| ||||| ||||||||||||||||||| ||||||||||||||
Db     721 TGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGATTAGATACCCTG 780

Qy     783 GTAGTCCACGCCGTAAACGATGTC--AACTAGTTGTTGGGCTTGGGCTTACTAGGCTTGGTAACGT 841
           |||||||||||||||||||| ||| |||||||||||| |||||||||||||||| |||||||||
Db     781 GTAGTCCACGCCGTAAACGATGTCGATTTGGAGGTTGTTGCCCGCAGAAGGCGTTAATCGTCGG 840

Qy     842 AGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAA 901
           |||||||||||| |||||||||||||||| |||||||||||||||||||||||||||||
Db     841 AGCTAACGCGTTAAATCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAA 900

Qy     902 TTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAAC 961
           ||||||||| ||||||||||||||| |||||||||||||||||||||||| ||||||||
Db     901 TTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAAC 960

Qy     962 CTTACCTACCCTTGACATGTAGCGATATTTAGAGATAAAATAGTGCCTTCGGGAACGC 1021
           ||||||| ||||||||||||||| |||||||||||||||||||||| |||||| ||||
Db     961 CTTACCTACTCTTGACATCCAGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTC 1020

Qy    1022 TAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCG 1081
           |||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db    1021 TGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCG 1080

Qy    1082 CAACGAGCGCAACCCTTGTCATTAGTTGCCATC-ATTTAGTTGGGCACTTTAATGAGACT 1140
           |||||||||||||| ||||||||||||||||| |||||| ||||||| |||||||||||
Db    1081 CAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCAAGGCCGGGAACTCAAAGGAGACT 1140

Qy    1141 GCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATCGGGTA 1200
           |||||| |||||||||||||||| |||||||||||||||||| ||||||||||| ||||
Db    1141 GCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTGCAC 1200
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Db

Qy    1201 GGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCGCGAGGGGGAGCTA 1260
           ||||| |||| ||||||||||||  ||||||||||||||||||||| ||||||||||
Db    1201 GGGCTACACACGTGCTACAATGGCGTATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGG 1260

Qy    1261 ATCTCAGAAAAGCGCGTCGTAGTCCGGATCGGAGTCGCAACTCGACTCCGTGAAGTCGGA 1320
           |||| ||||| |||| || |||||||||||  ||||||||||||||||||||||||||||
Db    1261 AACTCATAAAGTACGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGA 1320

Qy    1321 ATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACAC 1380
           ||||||||||||||||| |||| |||||||||||||||||||||||||||||||||||||
Db    1321 ATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGTTCCCGGGCCTTGTACACAC 1380

Qy    1381 CGCCCGTCACACCATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCGT-AAGAGGG 1439
           |||||||||||||| ||||||||||||| || ||||||| ||||| |||||| |||||||
Db    1381 CGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGTAGCTTAACCTTCGGGAGGGG 1440

Qy    1440 CGTTGCCACGGCGGAGATTCATGACTGG 1467
           || |||||||||||| ||||||||||||
Db    1441 CGCTTACCACTTTGTGATTCATGACTGG 1468
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RESULT 10
US-10-831-286A-48671
; Sequence 48671, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
;   APPLICANT: ZENG, QIANDONG
;   APPLICANT: CHATELLIER, SONIA
;   APPLICANT: MOIR, DONALD T.
;   APPLICANT: LACROIX, BRUNA
;   APPLICANT: CHILDRESS, DARRELL
;   TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
;   FILE REFERENCE: 032796-174.001
;   CURRENT APPLICATION NUMBER: US/10/831,286A
;   CURRENT FILING DATE: 2004-04-26
;   PRIOR APPLICATION NUMBER: 60/464,955
;   PRIOR FILING DATE: 2003-04-24
;   NUMBER OF SEQ ID NOS: 48788
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48671
;   LENGTH: 1530
;   TYPE: DNA
;   ORGANISM: Citrobacter youngae
US-10-831-286A-48671

Query Match   67.9%;   Score 995.8;   DB 9;   Length 1530;
Best Local Similarity   82.4%;   Pred. No. 8.5e-297;
Matches 1215;   Conservative   0;   Mismatches 252;   Indels   8;   Gaps   6;

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Qy       1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG 60
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||
Db       7 TTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAACGGTAG 66

Qy      61 CAC--GGGTGCTTGCACCT--GGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACG 116
           |||  |||||||||| ||  ||||||||||||||||||||||||||||||||||||||
Db      67 CACAGAGGAGCTTGCTCCTTGGGTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAAC 126

Qy     117 TGTTCCAGAAGTGGGGGATAACCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGA 176
           ||||||||||| |||||||||||||||||||||| ||||||||||| ||||||||||||
Db     127 TGCCCGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGA 186

Qy     177 GGAAAGCAGGGGATCGAAAGACCTTGTGCTTCGGGCGGTAAGTTAAGTCCG 236
           |||||| ||||||| ||| |||| |||||||||||||||||||||||||
Db     187 CCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATGGGATTAGCTAGT 246

Qy     237 TGGTGGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCC 296
           ||||||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     247 AGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCC 306

Qy     297 ACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGAC 356
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     307 ACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCAC 366
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Qy    1433  AAGAGGGGCGTTTGCCACGGCGAGAATTCATGACTGG 1467
            ||||||||   ||||||||||||||||||||||||||
Db    1447  GGGAGGGGCGGCCTTACCCACTTTGTGATTCATGACTGG 1481


RESULT 11
US-10-831-286A-48678
; Sequence 48678, Application US/10831286A
; Publication No. US2006004624 6A1
; GENERAL INFORMATION:
;  APPLICANT: ZENG, QIANDONG
;  APPLICANT: CHATELIER, SONIA
;  APPLICANT: MOIR, DONALD T.
;  APPLICANT: LACROIX, BRUNA
;  APPLICANT: CHILDRESS, DARRELL
;  TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
;  FILE REFERENCE: 037796-174.001
;  CURRENT APPLICATION NUMBER: US/10/831,286A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/464,955
;  PRIOR FILING DATE: 2003-04-24
;  NUMBER OF SEQ ID NOS: 48788
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48678
;  LENGTH: 1535
;  TYPE: DNA
;  ORGANISM: Proteus penneri
US-10-831-286A-48678

Query Match             67.4%;  Score 988.8;  DB 9;  Length 1535;
Best Local Similarity   81.6%;  Pred. No. 1.2e-294;
Matches 1205;  Conservative   0;  Mismatches 262;  Indels    9;  Gaps    5;

Qy      1  TTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTTTACACATGCAAGTCGAACGGCAG 60
           ||||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db      6  TTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAA 65

Qy     61  CA----CGGGTGCTTGCACCTGGTGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACG 116
           ||    |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66  CAGAAGAAAGCTTGCTTTCTTGCTGACGAGCGGCGGACGGGTGAGTAATGTATGGGGATC 125

Qy    117  TGTCCAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATAATTCTCTACGAG 176
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126  TGCCCGATAGAGGGGGATAACTACTGGAAACGGTGCTAATACCGCATAATGTCGCTACGGA 185

Qy    177  GGAAAGCAGGGGATCGAAAGACCTTGTCTTTGCGTATCGGATGAACCCATATGGATTAGT 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186  CCAAAGCAGGGGGTCTTCGGACCTTGCGCTATCGGATGAACCCATATGGGATTAGCTAGT 245

Qy    237  TGGTGGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCC 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246  AGGTGAGGTAAAGGCTCACCTAGGCGACGATCTCTAGCTGGTCTGAGAGGATGATCCAGCC 305

Qy    297  ACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGTGGGGAATTTTGGAC 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306  ACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGAATATTGCAC 365

Qy    357  AATGGGCGCAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAA 415
           |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db    366  AATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTAGGGTTGTAAA 425

Qy    416  GCTCTTTCAGTCGGGAGGAAGAAAAGGTTGTACTAAAT AATCACAACTTATGATGGTACCGAC 475
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426  GTACTTTCAGCGGGGAGGAAGGTGATAAAGTTAATACCTTTATCAATTGACGTTACCCGC 485

Qy    476  AGAAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTT 535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486  AGAAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTT 545

Qy    536  AATCGGAATTACTGGGCGTAAAGGGTCGGGCCTTTGTAAGTCAAGATGTGAAATCC- 1432
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546  AATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCAATTAAGTCAGATGTGAAAGCC 605
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Qy    357  AATGGGCGCAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAA 415
           |||||||||  |||||||||||||||||||||||||||||||||||  ||||||||||||||
Db    367  AATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAA 426

Qy    416  GCTCTTTCAGTCGGGAGGAAGAAAAGGTTGTTGACTAATAATCACAACTTATGATGGTACCGAC 475
           |||||||||||||||||||||||||||  |||||  |||||||||||||||||||||||||
Db    427  GTACTTTCAGCGGGGAGGAAGGGTTAATAACCTTATCCGGTGATGGTCTCGGTGAAATCC 486

Qy    476  AGAAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTT 535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487  AGAAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTT 546

Qy    536  AATCGGAATTACTGGGCGTAAAGGGTCGGGCCTTTGTAAGTCAAGATGTGAAATCC 595
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547  AATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAAGGC 606

Qy    596  CCGGGCTTAACCTGGGAATTGCGTTGAAACTACAAAGCTAGAGTGTAGCAGAGAGGGGGT 655
           ||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db    607  CCGGGCTCAACCTGGGAACTGCATCCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGT 666

Qy    656  GGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGC 715
           ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db    667  AGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGC 726

Qy    716  AGCCCCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGA 775
           ||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db    727  GGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGA 786

Qy    776  TACCCTGGTAGTCCACGCCCTAAACGATGTCAAC-TAGTTGTTGGGCCTTACTAGGCTTG 834
           ||||||||||||||||||||||||||||||     ||||||||||| ||||||||||||
Db    787  TACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGG 846

Qy    835  GTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTC 894
           |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db    847  CTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTC 906

Qy    895  AAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTGCCATCAACGC 954
           ||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db    907  AAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGC 966

Qy    955  GAAAAACCTTACCTACCCTTGACATGTGAGCGAATATTTAGAGATAAAATATGCCTTCG 1014
           ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db    967  GAAGAACCTTACCTACTCTTGACATCCAGAGAACTTAGCAGAGATGCTTTGGTGCCTTCG 1026

Qy   1015  GGAACGCTGAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAGATGTTGGGTTA 1074
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027  GGAACTGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTA 1086

Qy   1075  AGTCCCGCAACGAGCGCAACCCTTGTCATTAATTGCCATC-ATTTAGTTGGGCACTTTAA 1133
           ||||||||||||||||||||  |||||||||||||||||  |||||||||||||||||||
Db   1087  AGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCCGGCCGGGAACTCAAA 1146

Qy   1134  TGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTT 1193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147  GGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTT 1206

Qy   1194  ATGGGTAGGGCTTCACACGTAATACAATGGCGCGGTACAGAGGGCTGCCAACCCGCGAGGG 1253
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207  ACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAG 1266

Qy   1254  GGAGCTAATCTCAGAAAGCGCGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTCCGTGA 1313
           ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db   1267  CAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGA 1326

Qy   1314  AGTCGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGT 1373
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327  AGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGTTCCCGGGTCTTG 1386

Qy   1374  TACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGTTTAACCTT- 1432
           ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db   1387  TACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTC 1446
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;    CURRENT APPLICATION NUMBER: US/10/831,286A
;    CURRENT FILING DATE: 2004-04-26
;    PRIOR APPLICATION NUMBER: 60/464,955
;    PRIOR FILING DATE: 2003-04-24
;    SOFTWARE: PatentIn version 3.2
;    NUMBER OF SEQ ID NOS: 48788
;    SEQ ID NO 48681
;    LENGTH: 1494
;    TYPE: DNA
;    ORGANISM: Pantoea dispersa
US-10-831-286A-48681

Query Match             67.1%;    Score 984;  DB 9;   Length 1494;
Best Local Similarity   82.3%;    Pred. No. 3.7e-293;
Matches 1202; Conservative   0; Mismatches  250; Indels    8;  Gaps   6;

Qy      16 ATTGAACGCTGGGCGGCCATGCTTTACACATGCCAAGTCGAACGGCAGCACCG--GTGCTTGC    73
            ||||||||||||||||| |||||||||||||||||||||||||||||| |||   ||||||
Db       1 ATTGAACGCTGGGCGGCCAGGCCTAACACATGCAAGTCGAACGGCAGCGCAGAAGAGCTTGC    60

Qy      74 ACCT--GGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGG    131
            |||   |||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      61 TCTTTGGGTGGCGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCCGATGGAGGGG    120

Qy     132 GATAACGCATCGAAAGATGTCTAATACCGCATATTCTACGGAGGAAAGCAGGGGATC    191
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     121 GATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGTGGGGGACC    180

Qy     192 GAAAGACCTTGTCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGC    251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TTCGGGCCTTCACACCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGC    240

Qy     252 CTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCAGCCACACTGGGACTGAGA    311
            ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     241 TCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGA    300

Qy     312 CACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTGGACAATGGGCGAAAGCCT    371
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCT    360

Qy     372 GATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTGTAAAGCTCTTTCAGTCGAG    430
            ||||||||||| || |||||||||||||||| ||||||||||||||||||| |||||
Db     361 GATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGG    420

Qy     431 AAGAAAAGGTTGTGACTAATAATCACAACTTATGATGTGACAGAAGAAGCACCGGC    490
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AGGAAGGGGTGAGGTTAATAACCTCGCCGATTGACGTTACCCGCAGAAGAAGCACCGGC    480

Qy     491 TAACTACGTGCCAGCAGCCGCGGTAATACGTTCCCGGGTCTT    550
            |||||||||||||||||||||||||||||||||||||||||||
Db     481 TAACTCCGTGCCAGCAGCCGCGGTAATACGTTCCCGGGCCTT    540

Qy     551 GGTAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTG    610
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCAGATGTGAAATCCCCGGGCTTAACCTG    600

Qy     611 GAATTGCGTTGAAACTGCAAAGCTAGAGTAGTGCAGAGGGGTGGAATTCCATGTGTA    670
            ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GAACTGCATTTGAAACTGGCAGGCTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTA    660

Qy     671 GCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAA    730
            |||||||||||||||||||||| |||||||||||||||||||||||| ||||||||||
Db     661 GCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAAGCGGCAGATTAGATACCCTGGTAGTCCA    720

Qy     731 CACTGAGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA    790
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA    780

Qy     791 CGCCCTAAACGATGTCAACTAGTTGTTGGGCTTGG--TAACGTAGCTAACG    849
            |||||||||||||||||||||||| |||||| ||||   |||||||||||||
Db     781 CGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACG    840

Qy     850 CGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGAATTGACGGG    909
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Qy     596 CCGGGCTTAACCTGGGAATTGCGTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGT    655
            |||||||||||||||| |||||||||||||||     ||||||||| | |||||||||||
Db     606 CCGAGCTTAACCTGGGAATTGCGTTGAAACTGGTTGGATCTGAAACTGGCGTGAGGGGGT    665

Qy     656 GGAATTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGC    715
            ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db     666 AGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACCGGTGGCGAAGGC    725

Qy     716 AGCCCCCCTGGGTTAACTACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGA    775
            || |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     726 GGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGA    785

Qy     776 TACCCTGGTAGTCCACGCCCTAAACGATGTC-AACTAGTTGTTGGGCCTTACTAGGCTTG    834
            |||||||||||||||||||| ||||||||||| |||||||||||||||||| | |||||||
Db     786 TACCCTGGTAGTCCACGCCGTAAACGATGTCGATTTAGAGGTTGTGGTCTTGAACCGTGG    845

Qy     835 GTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTTACGGTCGCGAAGGATTAAAACTC    894
            || |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     846 CTTCTCGGAGCTAACGCGTTAAATCGACCGCCTGGGGAGTACGCCGGCAAGGTTAAAACTC    905

Qy     895 AAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGTTTAATTCGATGCAACGC    954
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db     906 AAATGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGC    965

Qy     955 GAAAAACCTTACCTACCCTTGACATGTAGCGGAATATTTTAGAGATAAAAATAGTGCCTTCG    1014
            |||||||||||||| ||||||||| || || ||||||||||||||| ||||||||||||||
Db     966 GAAGAACCTTACCTACTCTTGACATCCAGCGAATCCTTTAGAGATAGAGGAGTGCCTTCG    1025

Qy    1015 GGAACGCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAGATGTTGGGTTA    1074
            ||||||||||||||| ||||||||||||||||||||||||||||||| |||||||||||||
Db    1026 GGAACGCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTA    1085

Qy    1075 AGTCCCGCAACGAGCGCAACCCTTGTCATTTAGTTGCCA--TCATTTAGTTGGGCACTTTA    1132
            ||||||||||||||||||||||||| |||||| |||||||   |||||| ||||||||||||
Db    1086 AGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCGGGATGAACTGAACTCAA    1145

Qy    1133 ATGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCTCATGGCCCT    1192
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1146 AGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCT    1205

Qy    1193 TATGGGTAGGGCTTCACACGTGCTACAAGGTGCGGCGTACAGAGGGTTGCCAACCCGCGAGG    1252
            ||||||| | ||||||||||||| ||||||||||||||||||||||| |||||||||||||||
Db    1206 TACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGA    1265

Qy    1253 GGGAGCTAATCGACAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTG    1312
            |||||||||||| |  ||| || |||||||||| ||| |||||||||||||||||||||
Db    1266 GCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATG    1325

Qy    1313 AAGTCGGAATCGCTAGTAATCGCGGATCGCATGCCGCGGTGAATACGTTCCCGGGTCTT    1372
            |||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||||
Db    1326 AAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCGGGCCTT    1385

Qy    1373 GTACACACCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGT    1432
            |||||||||||||||||||||||||||||||||||| |||||| |||||||||||||||
Db    1386 GTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTT    1445

Qy    1433 -AAGAGGGCGTTTGCCACGGGCAGAATTCATGACTGG    1467
             |||||||||||||| |||||||||| | | ||||||||
Db    1446 CGGGAGGGCGCTTACCACTTTGTGATTCATGACTGG    1481
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RESULT 12
US-10-831-286A-48681
; Sequence 48681, Application US/10831286A
; Publication No. US2006004624A1
; GENERAL INFORMATION:
; APPLICANT:  ZENG, QIANDONG
; APPLICANT:  CHATELLIER, SONIA
; APPLICANT:  MOIR, DONALD T.
; APPLICANT:  LACROIX, BRUNA
; APPLICANT:  CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 02796-174.001
```

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Qy     1 GATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGGCGGTGTAAC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    62 ACGGGTGCTGCTGCAC----CTGGTGCGAGTGGCGCAGCGGCGGGTGAGTAATGCTCGGAACGT 117

Db    61 AGGGAGAAGCTTGCTTCTCTGCTGACGAGCGGCGGACGGGTGAGTAATGTATGGGGGATCT 120
         | |||||| ||||  |  | |  |||||||||||||||||||||||||||||||||||||||
Qy   118 GTCCAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAG 177

Qy   178 GAAAGCAGGGGATCGAAAGACCTTGTGCTTTGGAGAGCGGCCGATGCGGTGATTAGCTAGTT 237
         ||||||||||||||||||| |||||  | | | ||||||||||||||||||||||||||
Db   181 CAAAGCGGGGGACCTTCGGGCCTCGCGCCATCAGATGAACCCATATGGGATTAGCTAGTA 240

Db   241 GGTGAGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGATCAGCCA 300
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   298 CACTTGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACA 357

Qy   358 ATGGGCGAAAGCCTGATCCAGCCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAG 416
         |||||||||||||||||||||||||||||| |||||||||| || |||||| ||||||||
Db   361 ATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAG 420

Db   421 TACTTTCAGTCGGGAGGAAGGTGGTGCAAGGTTAATAACCTTGGCAATTGACGTTACCGACA 480
         |||| |||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Qy   477 GAAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTA 536

Qy   537 ATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGT-AAGAGGGCGTTTGCC 596
         ||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   541 ATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTTGATTGAGTCAGATGTGAAATCCC 600

Db   601 CGGGCTCAACCTGGGAATTGCATCTGATACTGGTCAGCTAGAGTGTGTAGAGGGGGGTA 660
         |||||||||||||||||||||||| ||| ||| ||||||||||||||||||
Qy   597 CGGGGCTTAACCTGGGAATTGCATTTGATACTGGGGAACTAGAGTGTGCAGAGGGGAGTG 656

Qy   657 GAATTCCATGTGTAGCGGTGAAATGCGTAGAGATATCGGAGGAACATCGACGGCGAAGGCG 716
         ||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   661 GAATTCCATGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCG 720

Qy   777 ACCTGGTAGTCCACGCCGTAAACGATGTCAAC-TAGTTGTTGGGCCTTACTAGGCTTGG 835
         ||||||||||||||||||| ||||| ||||| |||||||||||||||||||||||||
Db   781 ACCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGC 840

Qy   836 TAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGTTAAAACTCAA 895
         |||||||||||||||||  || |||||||||||||||||||||||| |||||||||||||
Db   841 TTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAA 900

Qy   896 AAGGAATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGCATGCAATTCGATGCAACGCG 955
         ||||||||||||||||| |||||||||||||||||| |||||||||||||||||||||||||
Db   901 AATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCG 960

Qy   956 AAAAACCTTACCTACCCTTGACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGG 1015
         ||||||||||||||||||||||||| |||| ||| ||||||||||||||||||||||||||
Db   961 AAGAACCTTACCTACTCTGACATCCAGAGAACTTTCCAGAGATGGGTTGGTGCCTTCGG 1020
```

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Db   841 CGTTAAGTCGACCGCCTGGGGAGTACGGTCGCAAGGTTAAAACTCAAATGAATTGACGGGG 900
Db   910 GACCCGCACAAGCGGTGGATTATGTGGAITAAGATAAAATAGTGCAACCTTACCTA 969
Db   901 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTG 960
Qy   970 CCCTTGACATAGTGAGATAATATTTAGAGATAAAATAGTGCCTTCGGGGACTCTCACAG 1029
Db   961 GCCTTGACATCCACAGAACTTTGGTGCCTTCGGGCGATCTCGAGACAG 1020
Qy  1030 GTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1089
Db  1021 GTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGC 1080
Qy  1090 GCAACCCCTTGTCATTAATTGCCATC-ATTTAGTTGGGCACTTTAATGAGACTGCCGGTGA 1148
Db  1081 GCAACCCTTATCCTTTGTTGCCAGCGGTTCGGCCGGGAACTCAAAGGAGACTGCCGGTGA 1140
Qy  1149 CAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGCCTAGGGCTTCA 1208
Db  1141 TAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACA 1200
Qy  1209 CACGTAATACAAATGGCGGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGA 1268
Db  1201 CACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATA 1260
Qy  1269 AAGCCGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAG 1328
Db  1261 AAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAG 1320
Qy  1329 TAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC 1388
Db  1321 TAATCGTGAATCAGAATGTCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC 1380
Qy  1389 ACACCATGGGAGTGGGTTTCACCAGAAGTAGTCTAACCGT-AAGGGGCGTTTGCC 1447
Db  1381 ACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACC 1440
Qy  1448 ACGGGCAGAGTTCATGACTGG 1467
Db  1441 ACTTTGTGATTCATGACTGG 1460
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RESULT 13
US-10-831-286A-48693
; Sequence 48693, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48693
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Morganella morganii sp. morganii
US-10-831-286A-48693

Query Match   67.1%;   Score 983.8;   DB 9;   Length 1527;
Best Local Similarity   81.9%;   Pred. No. 4.3e-293;
Matches 1208;   Conservative   0;   Mismatches 257;   Indels 10;   Gaps 6;

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Qy     3 GATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTA-CACATGCAAGTCGAACGGGCAGC 61
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Db   241 TCACCTAGGCGACGATCCTAGCTGGTCTGAGCAGCGATGACCAGCCACACTGGGAACTGAGA 300

Qy   312 CACGGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTGGACAATGGGCGAAAGCCT 371
         |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   301 CACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCT 360

Qy   372 GATCCAGCCAATGCCGCGTGAGTGAAGAAG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAG 430
         |||||||||||||||||||||||||||||| |||||| ||||||||||||||
Db   361 GATGCAGCCATGCCGCGTGTATGGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGG 420

Qy   431 AAGAAAGGTTGTGACTAATAATCACAACTTATGATGTGACGACAGAAGAAGCACCGGC 490
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGGAAGGCGGTGAGGTTAATAACCTTGCCGATTGACGTTACCCGCAGAAGAAGCACCGGC 480

Qy   491 TAACTACGTGCCAGCCGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG 550
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TAACTCCGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG 540

Qy   551 GCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGG 610
         ||||||||||||||||||||||||||||||||||||| ||| ||||
Db   541 GCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGG 600

Qy   611 GAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCATGTGTA 670
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GAACTGCATTTGAAACTGCAGGCTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTA 660

Db   671 GCAGTGAAATGCGTAGAGATATGCAGGAAGAACATCGATGGCGAAGGCAGCCCCTGGGTTAA 730
         || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCTGGACGAA 720

Qy   731 CACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA 790
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACACGATTAGATACCCTGGTAGTCCA 780

Qy   791 CGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGG-TAACGTAGCTAACG 849
         ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   781 CGCCGTAAACGATGTCGAGCATGTGTGTCCCTTGAGGCGTGCTTCCGGAGCTAACG 840

Qy   850 CGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGG 909
         ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   841 CGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGG 900

Qy   910 GACCCGCACAAGCGGTGGATTATGTGGGATTAATTGCAACGGCGAAAAACCTTACCTA 969
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTG 960

Qy   970 CCCTTGACATGCATGGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAG 1029
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   961 GCCTTGACATCCACGAGAACTTAGCAGAGATGCGTTTGGTGCCTTCGGGAACTCTGAGACAG 1020

Qy 1030 GTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1089
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db 1021 GTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGC 1080

Qy 1090 GCAACCCTTGTCATTAATTGCCATC-ATTTAGTTGGGCACTTTAATGACTGCCGGTGA 1148
         ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db 1081 GCAACCCTTATCCTTTGTTGCCAGCGGTTCGGCCGGGAACTCAAAGGAGACTGCCGGTGA 1140

Qy 1149 CAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTTAAGGGTTCA 1208
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACA 1200

Qy 1209 CACGTAATAACAATGGCGCGTACAGAGGGTTGCCAACCGCGAGAGGGGAGCTAATCTCAGA 1268
         |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 CACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATA 1260

Qy 1269 AAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAG 1328
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 AAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAG 1320

Qy 1329 TAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC 1388
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 TAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC 1380

Db 1081 GTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTTCGGCCGGGAACTCAAA 1140

Qy 1134 TGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTT 1193
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTT 1200

Qy 1194 ATGGGTTAGGGCTTCACACGTAATACAGAGGGTGGATAACGGCGTAATACAGAGGGTG 1253
         ||||||||| |||||||||||||||||||||||| |||| ||||||
Db 1201 ACGAGTAGGGCTACACACCGTGCTACAACGGCGTAATACCGAAGGAAGCGACCTCGCGAGAGC 1260

Qy 1254 GGAGCTAATCTCAGAAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGA 1313
         |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db 1261 CAAGCGGAACTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGA 1320

Qy 1314 AGTCGGAATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTG 1373
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 AGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCGGGCCTTG 1380

Qy 1374 TACACACCGCCCGTCACACCGATGGAGTGGTTTCACCAGAAGCAGTAGTCTAACC-GT 1432
         ||||||||||||||||| ||||||| ||| ||||
Db 1381 TACACACCGCCCGTCACACCATGGGAGTGGTTGCAAAAGAAGTAGTAGCTTAACCTTCC 1440

Qy 1433 AAGAGGGGCGTTTGCCACGGCCAGATTCATGACTGG 1467
         ||||||
Db 1441 GGGAGGGCGCTTACCACTTTGTGATTCATGACTGG 1475

RESULT 14
US-10-831-286A-48683
; Sequence 48683, Application US/10831286A
; Publication No. US2006004624 6A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48683
; LENGTH: 1493
; TYPE: DNA
; ORGANISM: Pantoea dispersa
US-10-831-286A-48683

Query Match   67.0%; Score 982.4; DB 9; Length 1493;
Best Local Similarity 82.3%; Pred. No. 1.2e-292;
Matches 1201; Conservative 0; Mismatches 251; Indels 8; Gaps 6;

Qy   16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGG--GTGCTTGC 73
         ||||||||||||||||||||| |||||||||||||||||||||||||| ||||||
Db   1 ATTGAACGCTGCGCGGCAGGCCTAAACACATGCAAGTCGAACGGCACACAGAGAGCTTGC 60

Qy   74 ACCT--GGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGG 131
         |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCTTTGGGTGGCGAGTGGCGAACGGGTGAGTAATGTCTGGGAAACTGCCCGATGAGGGGG 120

Qy   132 GATAACGCATCGAAAGATGTGCTAATAACGCTATATTCTTACGGAGGAAGAGCAGGGGATC 191
         |||| |||| ||||||||||||||||||||||||||||||||||||||
Db   121 GATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGTGGGGGACC 180

Qy   192 GAAAGACCTTGTCTTTGGAGCGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 251
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTCGGGCCTCACACCATCGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGC 240

Qy   252 CTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 311
         ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCACCTAGGCGACGATCCTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 300

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Qy   1389  ACACCATGGAGTGGGTTCACCAGAAGCAGATAGTCTAACCGT-AAGAGGGCGTTTGCC 1447
                  ||||||||||||  |||   |||   ||||||||||||||  ||||||  ||||||||
Db   1381  ACACCATGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACC 1440

Qy   1448  ACGGGCGAGATTCATGACTGG 1467
                  |||||||||||  |||||||
Db   1441  ACTTTGTGATTCATGACTGG 1460
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RESULT 15
US-10-831-286A-48676
; Sequence 48676, Application US/10831286A
; Publication No. US2006004246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48676
;   LENGTH: 1494
;   TYPE: DNA
;   ORGANISM: Enterobacter hormaechei
US-10-831-286A-48676

Query Match   66.7%; Score 979.2; DB 9; Length 1494;
Best Local Similarity 82.1%; Pred. No. 1.1e-291;
Matches 1199; Conservative 0; Mismatches 253; Indels 8; Gaps 6;

```
Qy     16  ATTGAACGCTGGCGCGCATGCTTACACATGCAAGTCGAACGGCAGCACG--GGTGCTTGC  73
               ||||||||||||||||||  |||||||||||||||||||||||||||||    |||||||
Db      1  ATTGAACGCTGGCGGCGCCAGGCCTAACACATGCAAGTCGAACGGTAACAGAAGCAGCTTGC  60

Qy     74  ACCT--GGTGCGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGG  131
              ||    || ||  ||||||||||  |||||||||||||||||||| ||   ||||||||||
Db     61  TGCTTCGCTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGG  120

Qy    132  GATAACGCATCGAAAGATGTGCTAATACCGCATATTTCTCTACGGAGGAAAGCAGGGGATC  191
              |||||||||||||||||  |||||||||||  |||  ||||||  ||||||||||||||||
Db    121  GATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACC  180

Qy    192  GAAAGACCTTGTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGC  251
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Qy    312  CACGGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT  371
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Qy   1209  CACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGA  1268
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Search completed: April 6, 2006, 21:15:08
Job time : 772 secs

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                    GenCore version 5.1.7
            Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:           April  6, 2006, 20:10:56 ; Search time 1287 Seconds
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Title:            US-10-659-983A-18
Perfect score:    1467
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Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters:       19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1467	100.0	1467	7	US-10-659-948A-18	Sequence 18, Appl
2	1467	100.0	1467	7	US-10-659-980A-18	Sequence 18, Appl
3	1467	100.0	1467	7	US-10-659-983A-18	Sequence 18, Appl
4	1440.2	98.2	1491	7	US-10-659-948A-20	Sequence 20, Appl
5	1440.2	98.2	1491	7	US-10-659-980A-20	Sequence 20, Appl
6	1440.2	98.2	1491	7	US-10-659-983A-20	Sequence 20, Appl
7	1403.4	95.7	1494	7	US-10-659-948A-19	Sequence 19, Appl
8	1403.4	95.7	1494	7	US-10-659-980A-19	Sequence 19, Appl
9	1403.4	95.7	1494	7	US-10-659-983A-19	Sequence 19, Appl
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13	1357.2	92.5	1457	7	US-10-659-948A-2	Sequence 2, Appli
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25	1151.8	78.5	1459	6	US-10-168-337A-8	Sequence 8, Appli
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31	1130.4	77.1	1426	6	US-10-168-337A-9	Sequence 9, Appl
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36	1103.4	75.2	1496	9	US-10-723-365B-32	Sequence 32, Appl
37	1101.6	75.1	1544	6	US-10-029-397A-45	Sequence 45, Appl
38	1101.6	75.1	2242716	9	US-10-915-740A-1068	Sequence 1068, Ap
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43	1095.2	74.7	1481	10	US-11-112-257-1	Sequence 1, Appli
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;  Sequence 18, Application US/10659948A
;  Publication No. US20040101946A1
;  GENERAL INFORMATION:
;  APPLICANT: Hovanec, Timothy A
;  TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
;  FILE REFERENCE: 81289-294309
;  CURRENT APPLICATION NUMBER: US/10/659,948A
;  CURRENT FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: US 09/573,684
;  PRIOR APPLICATION FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/386,217
;  PRIOR APPLICATION FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/386,218
;  PRIOR APPLICATION FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/386,219
;  PRIOR APPLICATION FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 23
;  SEQ ID NO 18
;  LENGTH: 1467
;  TYPE: DNA
;  ORGANISM: Unknown
;  FEATURE:
;  OTHER INFORMATION: N. Aestuarii-like AOB P4clone42 16S rDNA
US-10-659-948A-18

  Query Match             100.0%;  Score 1467;  DB 7;  Length 1467;
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  Matches 1467;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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RESULT 2
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; Sequence 18, Application US/10659980A
; Publication No. US2004010613A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 1467
; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: N. Aestuarii-like AOB P4clone42 16S rDNA
US-10-659-980A-18

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Db  1201 GGGCTTCACGCGTAATACAAGGGCGCTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTA 1260

Qy  1261 ATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCGCAACTCGACTCCGTGAAGTCGGA 1320
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Db  1261 ATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCGCAACTCGACTCCGTGAAGTCGGA 1320
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RESULT 3
US-10-659-983A-18

; Sequence 18, Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
;   APPLICANT: Hovanec, Timothy A
;   TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
;   FILE REFERENCE: 81289-284779
;   CURRENT APPLICATION NUMBER: US/10/659,983A
;   CURRENT FILING DATE:  2003-09-10
;   PRIOR APPLICATION NUMBER: US 09/573,684
;   PRIOR FILING DATE: 2000-05-19
;   PRIOR APPLICATION NUMBER: US 60/386,217
;   PRIOR FILING DATE: 2002-09-19
;   PRIOR APPLICATION NUMBER: US 60/386,218
;   PRIOR FILING DATE: 2002-09-19
;   PRIOR APPLICATION NUMBER: US 60/386,219
;   PRIOR FILING DATE: 2002-09-19
;   NUMBER OF SEQ ID NOS: 23
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 1467
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: N. Aestuarii-like AOB P4clone42 16S rDNA
US-10-659-983A-18

  Query Match             100.0%;  Score 1467;  DB 7;  Length 1467;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1467;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCGCAG   60
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Db      1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCGCAG   60

Qy     61 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  120
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Db     61 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  120

Qy    121 CAGAAGTGGGGGATAACGTCATGAAAGATGTGCTAATACCGCATATTCTCTACGGGAGGAA  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGAAGTGGGGGATAACGTCATGAAAGATGTGCTAATACCGCATATTCTCTACGGGAGGAA  180

Qy    181 AGCAGGGGATCGAAAGACCTTGTCGCTTTGGGAGCGGCCCGATGTCCTAATCAGTTAGTTGGT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGCAGGGGATCGAAAGACCTTGTCGCTTTGGGAGCGGCCCGATGTCCTAATCAGTTAGTTGGT  240

Qy    241 GGGGTAAAGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GGGGTAAAGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  300

Qy    301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360

Qy    361 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCT  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCT  420

Qy    421 TTCAGTCGAGAGAAAGGTTGTGACTAATAATCACAACTTATGATGTACCGACAGAGAAG  480
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Db    421 TTCAGTCGAGAGAAAGGTTGTGACTAATAATCACAACTTATGATGTACCGACAGAGAAG  480

Qy    481 AAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCG  540
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Db    481 AAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCG  540

Qy    541 GAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGG  600

Qy    601 CTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAAT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAAT  660

Qy    661 TCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCC  720
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Db    661 TCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCC  720

Qy    721 CCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCC  780
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Db    721 CCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCC  780

Qy    781 TGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGGTAACG  840
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Db    781 TGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGGTAACG  840

Qy    841 TAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAAGGA  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAAGGA  900

Qy    901 ATTGACGGGGACCCGCACAAGCGGTGGATTAATGTGATGGAATTCGATGCAACGCGAAAA  960
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Db    901 ATTGACGGGGACCCGCACAAGCGGTGGATTAATGTGATGGAATTCGATGCAACGCGAAAA  960

Qy    961 CCTTACCTACCCTTGACATGTTAGCATGTTTAGAGATAAATAGTGCCTTCGGGAACG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CCTTACCTACCCTTGACATGTTAGCATGTTTAGAGATAAATAGTGCCTTCGGGAACG 1020

Qy   1021 CTAACACAGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CTAACACAGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC 1080

Qy   1081 GCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACT 1140

Qy   1141 GCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTA 1200

Qy   1201 GGGCTTCACACGTAATACAATGGCCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGGCTTCACACGTAATACAATGGCCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTA 1260

Qy   1261 ATCTCAGAAAGCCGGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGA 1320
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Db   1261 ATCTCAGAAAGCCGGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGA 1320

Qy   1321 ATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACAC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACAC 1380

Qy   1381 CGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGCAGAGTAGTCTAACCGCAAGGGC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGCAGAGTAGTCTAACCGCAAGGGC 1440

Qy   1441 GTTTGCCACGGCGAGATTCATGACTGG 1467
          |||||||||||||||||||||||||||
Db   1441 GTTTGCCACGGCGAGATTCATGACTGG 1467
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;  PRIOR APPLICATION NUMBER: US 60/386,217
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/386,218
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/386,219
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 20
;  LENGTH: 1491
;  TYPE: DNA
;  ORGANISM: Unknown
;  FEATURE:
;  OTHER INFORMATION: N. Aestuarii-like AOB BF16clone57 16S rDNA
US-10-659-948A-20

Query Match             98.2%;  Score 1440.2;  DB 7;  Length 1491;
Best Local Similarity   99.7%;  Pred. No. 0;
Matches 1464;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy      1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCGCAG 60
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Db      3 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCGCAG 62

Qy     61 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTC 120
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Db     63 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTC 122

Qy    121 CAGAAGTGGGGGATAACGATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 CAGAAGTGGGGGATAACGATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA 182

Qy    181 AGCAGGGGATCGAAAGACCTTGTCGTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT 240
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Db    183 AGCAGGGGATCGAAAGACCTTGTCGTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT 242

Qy    241 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC 300
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Db    243 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC 302

Qy    301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 362

Qy    361 GGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAG-CTTCGGGTTGTAAAGCTC 419
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    363 GGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGCCCTTCGGGTTGTAAAGCTC 422

Qy    420 TTTCAGTCGAGAGAAAAGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA 479
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    423 TTTCAGTCGAGAGAAAAGTTGTGACTAATAATCACAACTTATGACGGTACCGACAGAA 482

Qy    480 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 539
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 542

Qy    540 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGG 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGG 602

Qy    600 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAA 659
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAA 662

Qy    660 TTTCCATGTGTAGCAGTGAAATGCGTAGATATGGAAGAACATCGATGGCGAAGGCAGCC 719
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    663 TTTCCATGTGTAGCAGTGAAATGCGTAGATATGGAAGAACATCGATGGCGAAGGCAGCC 722

Qy    720 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 779
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Db    723 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 782

Qy    780 CTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC 839
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Qy    601 CTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAAT 660
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Db    601 CTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAAT 660

Qy    661 TCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCC 720

Qy    721 CCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCC 780
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Db    721 CCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCC 780

Qy    781 TGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACG 840

Qy    841 TAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGA 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    841 TAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAAACTCAAAGA 900

Qy    901 ATTGACGGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTGACGGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA 960

Qy    961 CCTTACCTACCCTTGACATGCATGGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACG 1020
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Db    961 CCTTACCTACCCTTGACATGCATGGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACG 1020

Qy   1021 CTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC 1080

Qy   1081 GCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTTAGTTGGGCACTTTAATGAGACT 1140
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Db   1081 GCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTTAGTTGGGCACTTTAATGAGACT 1140

Qy   1141 GCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTA 1200
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Db   1141 GCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTA 1200

Qy   1201 GGGCTTCACACGGTCTAATACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTA 1260
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Db   1201 GGGCTTCACACGGTCTAATACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTA 1260

Qy   1261 ATCTCAGAAAGCCGGTCGTAGTTCGGATCGCGAGTCTGCAACTCGACTCGTGAAGTCGGA 1320
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Db   1261 ATCTCAGAAAGCCGGTCGTAGTTCGGATCGCGAGTCTGCAACTCGACTCGTGAAGTCGGA 1320

Qy   1321 ATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACAC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACAC 1380

Qy   1381 CGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAAGGGGGC 1440
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Db   1381 CGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAAGGGGGC 1440

Qy   1441 GTTTGCCACGGCCGAGATTCATGACTGG 1467
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Db   1441 GTTTGCCACGGCCGAGATTCATGACTGG 1467
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; OTHER INFORMATION: N. Aestuarii-like AOB BF16clone57 16S rDNA
US-10-659-980A-20

Query Match   98.2%;   Score 1440.2;   DB 7;   Length 1491;
Best Local Similarity   99.7%;   Pred. No. 0;
Matches 1464;   Conservative 2;   Mismatches 0;   Indels 3;   Gaps 2;

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Qy    1  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG   62

Qy   61  CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63  CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  122

Qy  121  CAGAAGTGGGGGATAACGATCAGAAGATGTCTAATACCGCATATTCTCTACGGAGGAA   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  123  CAGAAGTGGGGGATAACGATCAGAAGATGTCTAATACCGCATATTCTCTACGGAGGAA   182

Qy  181  AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  183  AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT  242

Qy  241  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  300
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Db  243  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  302

Qy  301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  303  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  362

Qy  361  GGGGAAACCTGATCCAGCCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTC  419
         ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  363  GGGGAAACCTGATCCAGCCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTC  422

Qy  420  TTTCAGTCGAGAGAAAAAGGTTGTGACTAATAATCACAACTACAAGCTAGAGTGTAGCAGAA  479
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Db  423  TTTCAGTCGAGAGAAAAAGGTTGTGACTAATAATCACAACTACAAGCTAGAGTGTAGCAGAA  482

Qy  480  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  539
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Db  483  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  542

Qy  540  GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTGTTAAGTCAGATGTGAAATCCCCGG  599
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Db  543  GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTGTTAAGTCAGATGTGAAATCCCCGG  602

Qy  600  GCTTAACCTGGGAATTGCGTTTGAAAACTACAAAGCTAGAGTGTCAGAGAGGGGTGGAA  659
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Db  603  GCTTAACCTGGGAATTGCGTTTGAAAACTACAAAGCTAGAGTGTCAGAGAGGGGTGGAA  662

Qy  660  TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC  719
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Db  663  TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC  722

Qy  720  CCCTGGGTTAACACTGACGCTCATGCAGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC  779
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  723  CCCTGGGTTAACACTGACGCTCATGCAGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC  782

Qy  780  CTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCGTTCGCAGGGATTAAAACTCAAAGG  839
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  783  CTGGTAGTCAACGCGCCTAAACGATGTCAACTAGTTGTTGGGCGTTCGCAGGGATTAAAACTCAAAGG  842

Qy  840  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  899
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Db  843  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  902

Qy  900  AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  959
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  903  AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  962

Qy  960  ACCTTACCTACCCTTGACATGTAGCGAATATTTAGAGATAAAAATAGTGCCTTCGGGAAC 1019
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  963  ACCTTACCTACCCTTGACATGTAGCGAATATTTAGAGATAAAAATAGTGCCTTCGGGAAC 1022

Qy 1020  GCTAACACAGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1079
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1023  GCTAACACAGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1082

Qy 1080  CGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGCACTTTAATGAGAC  1139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1083  CGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGCACTTTAATGAGAC  1142

Qy 1140  TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT  1199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1143  TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT  1202

Qy 1200  AGGGCCTTACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT  1259
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1203  AGGGCCTTACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT  1262

Qy 1260  AATCTCAGAAAGCGCGTCGTAGTCCGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGG  1319
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1263  AATCTCAGAAAGCGCGTCGTAGTCCGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGG  1322

Qy 1320  AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACA  1379
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1323  AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACA  1382

Qy 1380  CCGCCCGTCACACCATGGGAGTTGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGG  1438
         |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db 1383  CCGCCCGTCACACCATGGGAGTGGTTTCACCAGAAGCAGATAGTCTAACCGTAAGGAGG  1442

Qy 1439  GCGTTTGCCACGGCGAGATTCATGACTGG  1467
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Db 1443  GCGTTTGCCACGGCGAGATTCATGACTGG  1471
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RESULT 5
US-10-659-980A-20
; Sequence 20, Application US/10659980A
; Publication No. US20040106113A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR APPLICATION FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR APPLICATION FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR APPLICATION FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR APPLICATION FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:

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Db    63  CACGGGTGCTTGCACCTGGTGCGGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  122
Db   123  CACGGGTGCTTGCACCTGGTGCGGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC 1202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   121  CAGAAGTGGGGATAACGTCTCGAAAGATGTCTAATACCGCATATTCTCTACGGAGGAA  180
Db   123  CAGAAGTGGGGATAACGTCTCGAAAGATGTCTAATACCGCATATTCTCTACGGAGGAA  182

Qy   181  AGCAGGGGATCGAAAGACCTTGCTGTTTGGAGCGGCCGATGGCGATTAGCTAGTTGGT  240
Db   183  AGCAGGGGATCGAAAGACCTTGCTGTTTGGAGCGGCCGATGGCGATTAGCTAGTTGGT  242

Qy   241  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  300
Db   243  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  302

Qy   301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
Db   303  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  362

Qy   361  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTC  419
Db   363  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTC  422

Qy   420  TTTCAGTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGTGACCGACAGAA  479
Db   423  TTTCAGTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGTGACCGACAGAA  482

Qy   480  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAAGCGTTAATC  539
Db   483  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAAGCGTTAATC  542

Qy   540  GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAGCAGAAGAC  599
Db   543  GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAGCAGAAGAC  602

Qy   600  GCTTAACCTTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA  659
Db   603  GCTTAACCTTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA  662

Qy   660  TTCCATGTGTAGCAGTGAAATGCGTAGAGATCATGCAGGAACATCATGGGAAGGCAGCC  719
Db   663  TTCCATGTGTAGCAGTGAAATGCGTAGAGATCATGCAGGAACATCATGGGAAGGCAGCC  722

Qy   720  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC  779
Db   723  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC  782

Qy   780  CTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGGCCTTACTAGGCTTGGTAAC  839
Db   783  CTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGGCCTTACTAGGCTTGGTAAC  842

Qy   840  GTAGCTAACGGGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  899
Db   843  GTAGCTAACGGGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  902

Qy   900  AATTGACGGGGACCCGCACAAGCGGTGGATTAATTCGATGCAACGCGAAAA  959
Db   903  AATTGACGGGGACCCGCACAAGCGGTGGATTAATTCGATGCAACGCGAAAA  962

Qy   960  ACCTTACCTACCCTTGACATGCTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC  1019
Db   963  ACCTTACCTACCCTTGACATGCTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC  1022

Qy  1020  GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1079
Db  1023  GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1082

Qy  1080  CGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGCACTTTAATGAGAC  1139
Db  1083  CGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGCACTTTAATGAGAC  1142

Qy  1140  TGCCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT  1199
Db  1143  TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT  1202
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Db   963  ACCTTACCTACCCTTGACATGCTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC  1022
Qy  1020  GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1079
Db  1023  GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1082

Qy  1080  CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGAC  1139
Db  1083  CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGAC  1142

Qy  1140  TGCCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT  1199
Db  1143  TGCCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT  1202

Qy  1200  AGGGCTTCACACGTGATAATACAATGGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT  1259
Db  1203  AGGGCTTCACACGTAATAACAATGGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT  1262

Qy  1260  AATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTTCTGCAACTCGACTCCGTGAAGTCCG  1319
Db  1263  AATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTTCTGCAACTCGACTCCGTGAAGTCCG  1322

Qy  1320  AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACA  1379
Db  1323  AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACA  1382

Qy  1380  CCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGG  1438
Db  1383  CCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAAGGAGG  1442

Qy  1439  GCGTTTGCCACGGCGGAGATTCATGACTGG  1467
Db  1443  GCGTTTGCCACGGCGGAGATTCATGACTGG  1471
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RESULT 6
US-10-659-983A-20
; Sequence 20, Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
;   APPLICANT: Hovanec, Timothy A
;   TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
;   FILE REFERENCE: 81289-284779
;   CURRENT APPLICATION NUMBER: US/10/659,983A
;   CURRENT FILING DATE: 2003-09-10
;   PRIOR APPLICATION NUMBER: US 09/573,684
;   PRIOR FILING DATE: 2000-05-19
;   PRIOR APPLICATION NUMBER: US 60/386,217
;   PRIOR FILING DATE: 2002-09-19
;   PRIOR APPLICATION NUMBER: US 60/386,218
;   PRIOR FILING DATE: 2002-09-19
;   PRIOR APPLICATION NUMBER: US 60/386,219
;   PRIOR FILING DATE: 2002-09-19
;   NUMBER OF SEQ ID NOS: 23
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 1491
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: N. Aestuarii-like AOB BF16clone57 16S rDNA
US-10-659-983A-20

Query Match   98.2%; Score 1440.2; DB 7; Length 1491;
Best Local Similarity   99.7%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy    1  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG  60
Db    3  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG  62

Qy   61  CACGGGTGCTTGCACCTGGTGCGGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  120
Db   63  CACGGGTGCTTGCACCTGGTGCGGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  122
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Qy   301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   304 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAACG 363

Qy   361 GGCGAAAGCCTGATCCAGCAATCGCCGCGTGAGTGGAAGAAGG-CTTCGGCGGTTGTAAAGCTC 419
         ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   364 GGCGAAAGCCTGATCCAGCAATCGCCGCGTGAGTGGAAGAAGGCCTTCGGCGGTTGTAAAGCTC 423

Qy   420 TTTCAGTCGAGAAGAAAAGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA 479
         ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   424 TTTCAGTCGAGAAGAAAAGTTGTGACTAATAATCAACTTATGATGGTACCGACAGAA 483

Qy   480 GAAGCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 539
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   484 GAAGCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 543

Qy   540 GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGCTTGTTAAGTCAGATGTGAAATCCCCG 599
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGCTTGTTAAGTCAGATGTGAAATCCCCG 603

Qy   600 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAA 659
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAA 663

Qy   660 TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC 719
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664 TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC 723

Qy   720 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 779
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   724 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 783

Qy   780 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC 839
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   784 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC 843

Qy   840 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGTCGCAAGATTAAAACTCAAAGG 899
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   844 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGTCGCAAGATTAAAACTCAAAGG 903

Qy   900 AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAA 959
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   904 AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAA 963

Qy   960 ACCTTACCTACCCTTGACATGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1019
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964 ACCTTACCTACCCTTGACATGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1023

Qy  1020 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1079
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1024 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1083

Qy  1080 CGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGCACTTTAATGAGAC 1139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1084 CGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGCACTTTAATGAGAC 1143

Qy  1140 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCAAGGCCCTTATGGGT 1199
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1144 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCAAGGCCCTTATGGGT 1203

Qy  1200 AGGGCTTCACACGTAATACAATGGCGGTAATACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1259
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1204 AGGGCTTCACACGTAATACAATGGCGGTAATACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1263

Qy  1260 AATCTCAGAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACTCCGTGAAGTCGG 1319
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1264 AATCTCAGAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACTCCGTGAAGTCGG 1323

Qy  1320 AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1379
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1324 AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1383
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Qy  1200 AGGGCTTCACACGTAATACAATGGCGGTAATACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1259
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1203 AGGGCTTCACACGTAATACAATGGCGGTAATACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1262

Qy  1260 AATCTCAGAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACTCCGTGAAGTCGG 1319
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1263 AATCTCAGAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACTCCGTGAAGTCGG 1322

Qy  1320 AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1379
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1323 AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1382

Qy  1380 CCGCCCGTCACACCATGGGAGTGGGTTCCACCAGAAGCAGCAGATAGTCTAACCGTAA-GAGG 1438
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  1383 CCGCCCGTCACACCATGGGAGTGGGTTCCACCAGAAGCAGCAGATAGTCTAACCGTAAGAGG 1442

Qy  1439 GCGTTTGCCACGGCGGAGATTCATGACTGG 1467
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Db  1443 GCGTTTGCCACGGCGGAGATTCATGACTGG 1471
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RESULT 7
US-10-659-948A-19
; Sequence 19, Application US/10659948A
; Publication No. US2004010194G6A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: N. Aestuarii-like AOB P4clone31 16S rDNA
US-10-659-948A-19

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Query Match    95.7%;    Score 1403.4;    DB 7;    Length 1494;
Best Local Similarity    98.1%;    Pred. No. 0;
Matches 1441;    Conservative    0;    Mismatches    26;    Indels    2;    Gaps    2;

Qy     1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG 60
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Db     4 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG 63

Qy    61 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    64 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC 123

Qy   121 CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA 180
         | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124 CGGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA 183

Qy   181 AGCAGGGGATCGAAAGACCTTGTGCTTTGCTTTGCGCGGGAGCCGGATGCCTGATTAGCTAGTTGGT 240
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Db   184 AGCAGGGGATCGAAAGACCTTGTGCTTTGCTTTGCGCGGGAGCCGGATGCCTGATTAGCTAGTTGGT 243

Qy   241 GGGGTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTGGTTGTCTGAGAGGACGACCAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244 GGGGTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTGGTTGTCTGAGAGGACGACCAC 303
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Qy 480 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 539
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 484 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 543

Qy 540 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGG 599
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 544 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGG 603

Qy 600 GCTTAACCTGGGAATTGCGTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA 659
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 604 GCTTAACCTGGGAATTGCGTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA 663

Qy 660 TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC 719
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Db 664 TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC 723

Qy 720 CCCTGGGTAACACTGACGCTCATGCACGAAAGGGTGGGAGCAAACAGATTAGATACC 779
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 724 CCCTGGGTAACACTGACGCTCATGCACGAAAGGGTGGGAGCAAACAGATTAGATACC 783

Qy 780 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGGCCTTACTAGGCTTCGTAAC 839
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Db 784 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGGCCTTACTAGGCTTCGTAAC 843

Qy 840 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG 899
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Db 844 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG 903

Qy 900 AATTGACGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA 959
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 904 AATTGACGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA 963

Qy 960 ACCTTACCTACCCTTGACATGTAGCGGAATATTTAGAGATAAAAATAGTGCCTTCGGGAAC 1019
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 964 ACCTTACCTACCCTTGACATGTAGCGGAATATTTAGAGATAAAAATAGTGCCTTCGGGAAC 1023

Qy 1020 GCTAACACAGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1079
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1024 GCTAACACAGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1083

Qy 1080 CGCAACGAGCGCAACCCTTGTCATTATTGCCATCATTAGTTGGGCACTTAATGAGAC 1139
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1084 CGCAACGAGCGCAACCCTTGTCATTATTGCCATCATTAGTTGGGCACTTAATGAGAC 1143

Qy 1140 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGGCCCTTATGGGT 1199
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1144 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGGCCCTTATGGGT 1203

Qy 1200 AGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1259
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1204 AGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1263

Qy 1260 AATCTCAGAAAGCGCGTCGTAGTCCGGATCGCAGTCCGGATGCGTAGTCCGATCAGACTCGG 1319
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1264 AATCTCAGAAAGCGCGTCGTAGTCCGGATCGCAGTCCGGATGCGTAGTCCGATCAGACTCGG 1323

Qy 1320 AATCGCTAGTAATCGCGGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1379
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1324 AATCGCTAGTAATCGCGGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1383

Qy 1380 CCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGT-AAGAGG 1438
        ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db 1384 CCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGT-AAGAGG 1443

Qy 1439 GCGTTTGCCACGGCGAGATTCATGACTGG 1467
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Db 1444 ACGCTTACCACCGGTGTGGTCAATGACTTG 1472

Query Match   95.7%; Score 1403.4; DB 7; Length 1494;
Best Local Similarity   98.1%; Pred. No. 0;
Matches 1441; Conservative 0; Mismatches 26; Indels 2; Gaps 2;

Qy   1 TTGATCATGGTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4 TTGATCATGGTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG 63

Qy 61 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAAGTGTC 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 64 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC 123

Qy 121 CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 124 CGGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA 183

Qy 181 AGCAGGGGATCGAAAGACCTTGTCTTTGGAGCGGCCGATGCCGATGCCGATCAGACTCGG 240
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 184 AGCAGGGGATCGAAAGACCTTGTCTTTGGAGCGGCCGATGCCGATGCCGATCAGACTCGG 243

Qy 241 GGGGACTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTGGAGTAAAGCTC 300
       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 244 GGGGACTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTGGAGTAAAGCTC 303

Qy 301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAACG 360
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 304 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAACG 363

Qy 361 GGCGAAAGCCTGATCCAGCCATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTC 419
       ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db 364 GGCGAAAGCCTGATCCAGCCATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTC 423

Qy 420 TTTCAGTTCGAGAGAAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA 479
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 424 TTTCAGTTCGAGAGAAAAGGTTGTGACTAATAATCACAACTTATGACGGTACCGACAGAA 483

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; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284779
; CURRENT APPLICATION NUMBER: US/10/659,983A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 19
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: N. Aestuarii-like AOB P4clone31 16S rDNA
US-10-659-983A-19

Query Match        95.7%;   Score 1403.4;   DB 7;   Length 1494;
Best Local Similarity   98.1%;   Pred. No. 0;
Matches 1441;  Conservative   0;  Mismatches   26;  Indels   2;  Gaps   2;

Qy      1  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG   60
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      4  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG   63

Qy     61  CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64  CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  123

Qy    121  CAGAAGTGGGGGATAACGCATCGAAAGATGTCTAATACCGCATATTCTCTACGGAGGAA  180
           || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124  CGGAAGTGGGGGATAACGCATCGAAAGATGTCTAATACCGCATATTCTCTACGGAGGAA  183

Qy    181  AGCAGGGGATCGAAAGACCTTGTCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184  AGCAGGGGATCGAAAGACCTTGTCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT  243

Qy    241  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  303

Qy    301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    304  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAACG  363

Qy    361  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGGTTGTAAAGCTC  419
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    364  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGGTTGTAAAGCTC  423

Qy    420  TTTCAGTCGAGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGATGGTACCGACAGAA  479
           ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    424  TTTCAGTCGAGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGACGGTGCAAGCGTTAATC  483

Qy    480  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGGAGGGTGCAAGCGTTAATC  539
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGGAGGGTGCAAGCGTTAATC  543

Qy    540  GGAATTACTGGGCGTAAAGGGCGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGG  599
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    544  GGAATTACTGGGCGTAAAGGGCGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGG  603

Qy    600  GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGTGGAA  659
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604  GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAA  663

Qy    660  TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCC  719
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Db    664  TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCC  723
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    720  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACC  779
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACC  783

Qy    780  CTGGTAGTCCAGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC  839
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784  CTGGTAGTCCAGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC  843

Qy    840  GTAGCTAACGCGTGAAGTTGACCGCCTCGGGGAGTACGTCGCAGAGATTAAAACTCAAAGG  899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844  GTAGCTAACGCGTGAAGTTGACCGCCTCGGGGAGTACGTCGCAAGATTAAAACTCAAAGG  903

Qy    900  AATTGACGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  959
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904  AATTGACGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  963

Qy    960  ACCTTACCTACCCTTGACATGTGAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAC  1019
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964  ACCTTACCTACCCTTGACATGTGAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAC  1023

Qy   1020  GCTAACACAGAGTGCTGCATGCGTGTCGTCGAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1079
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024  GCTAACACAGAGTGCTGCATGCGTGTCGTCGAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1083

Qy   1080  CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTAATGAGAC  1139
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084  CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTAATGAGAC  1143

Qy   1140  TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCATGCCCTTATGGGT  1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144  TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCATGCCCTTATGGGT  1203

Qy   1200  AGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT  1259
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204  AGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT  1263

Qy   1260  AATCTCAGAAAGCGCGTCGTAGTCCGGATCAGCAGTCTGCGGATCGGGAGTCGTGAAGTCGG  1319
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264  AATCTCAGAAAGCGCGTCGTAGTCCGGATCAGCAGTCTGCGGATCGGGAGTCGTGAAGTCGG  1323

Qy   1320  AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGTCTTGTACACA  1379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324  AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACA  1383

Qy   1380  CCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGAGTAGTGTCTAACCGT-AAGAGG  1438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1384  CCGCCCGTCACACCATGGGAGTGGGTTGGCTGCACCAGAAGTAGGGTGTCTAACCCTCGGGAGG  1443

Qy   1439  GCGTTTGCCACGGCGAGATTCATGACTGG  1467
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Db   1444  ACGCTTACCACGGCGTGCTCAATGACTTG  1472
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RESULT 10
US-10-659-948A-1
; Sequence 1, Application US/1065994BA
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
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; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AOB Type A R7clone140 16S rDNA
US-10-659-948A-1

  Query Match     92.6%;  Score 1358.8;  DB 7;  Length 1457;
  Best Local Similarity   97.2%;  Pred. No. 0;
  Matches 1414;  Conservative   0;  Mismatches  37;  Indels   3;  Gaps   3;
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Qy    16 ATTGAACGCTGGCGGCATGCTTTACACATCGCAAGTCGAACGGCAGCACGGGTGCTTGCAC  75
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATTGAACGCTGGCGGCATGCTTTACACATCGCAAGTCGAACGGCAGCACGGATGCTTGCAT  60

Qy    76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA  135
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTATCCAGAGAGAGGGGGGTA  120

Qy   136 ACGCATCGAAAGATGTCGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA  195
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACGCATCGAAAGATGTCGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA  180

Qy   196 GACCTTGTGCTTTTGAGCGGCCGATGCGCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC  255
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GACCTTGCGCTTTTGAGCGGCCGATGCGCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC  240

Qy   256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  315
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  300

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGGAAAGCCTGATC  375
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC  360

Qy   376 CAGCAATGCCGCGTGAGTGAAGAAG-CTTCGGGGTTGTAAAGCTCTTTCAGTCGAGAAGA  434
         |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db   361 CAGCAATGCCGCGTGAGTGAAGAAGAAGCTTCGGGGTTGTAAAGCTCTTTCAGTCGAGAAGA  420

Qy   435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC  494
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAAGGTTACGGTAAATAATCGTGACTCATGACGTATCGACAGAAGAAGCACCGGCTAAC  480

Qy   495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  554
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  540

Qy   555 AAAGGGTGCGCAGGCGGCCGGCTTTGTAAGTGTGTCAGATGTGAAATCCCGGGGCTTGGAAT  614
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGGGTGCGCAGGCGGCCGGCTTTGTAAGTGTGTCAGATGTGAAATCCCGGGGCTTGGAAT  600

Qy   615 TGCGGTTTGAAACTACAAAGCTAGAGTGTGTGCAGAGGGGGTGGAATTCCATGTGTAGCAG  674
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGCGGTTTGAAACTACAAGGCTAGAGTGTGTGCAGAGGGGGTGGAATTCCATGTGTAGCAG  660

Qy   675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCCTGGGCTTAACACT  734
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCCTGGGCTTAACACT  720

Qy   735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  794
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  780

Qy   795 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTCGTAACGTAGCTAACGCGTGA  854
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCTTCGTAACGTAGCTAACGCGTGA  840

Qy   855 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC  914
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC  900

Qy   915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  974
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  960

Qy   975 GACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT  1034
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC-TTCGGAACGCTAACACAGGTGCT  1019

Qy  1035 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC  1094
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1020 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC  1079

Qy  1095 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTAATGAGACTGCCGGTGACAAACC  1154
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1080 CCTTGTCATTAATTGCCATCATTTGGTTGGGCACTTAATGAGACTGCCGGTGACAAACC  1139

Qy  1155 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGGCCCTTATGGGTAGGGGCTTCACGTA  1214
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGGCCCTTATGGGTAGGGGCTTCACGTA  1199

Qy  1215 ATACAATGGCGCGTACAGAGGGTTGCCAACACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC  1274
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 ATACAATGGCGCGTACAGAGGGTTGCCAACACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC  1259

Qy  1275 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG  1334
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1260 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG  1319

Qy  1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA  1394
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA  1379

Qy  1395 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGGCG  1453
         ||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db  1380 TGGGAGTGGGTTTCACCAGAAGCAGGTAGTCTAACCGTAACCGTAAGAGGGCGTTTGCCACGGTG  1439

Qy  1454 AGATTCATGACTGG  1467
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Db  1440 AGATTCATGACTGG  1453
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RESULT 11
US-10-659-980A-1
; Sequence 1, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AOB Type A R7clone140 16S rDNA
US-10-659-980A-1

  Query Match     92.6%;  Score 1358.8;  DB 7;  Length 1457;
  Best Local Similarity   97.2%;  Pred. No. 0;
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Matches 1414;  Conservative 0;  Mismatches 37;  Indels 3;  Gaps 3;

Qy    16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCACGGCACGGGTGCTTGCAC  75
         |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCGGCACGGGTGCTTGCAT  60

Qy    76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA 135
         |||||||||||||||||||||||||||||||||||||||||||
Db    61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGAACGGGAACGGGGGGTA 120

Qy   136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 195
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 180

Qy   196 GACCTTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
         ||||||| |||||||||||||||| ||||||||||||||||||||||||||||||||
Db   181 GACCTTGCGCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 240

Qy   256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 315
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 300

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
         |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC 360

Qy   376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTGTAAAGCTCTTTCAGTTCGAGAAGA 434
         ||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db   361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTGTAAAGCTCTTTCAGTTCGAGAAGA 420

Qy   435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC 494
         ||||||| |  |||||||| |  ||| |  | ||||| ||||||||||||||||||||||
Db   421 AAAGGTTACGGTAAATAATCGTGACTCATCAGACGGTATCGACAGAAGAAGCACCGGCTAAC 480

Qy   495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 540

Qy   555 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 614
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 600

Qy   615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGAATTCCATGTGTAGCAG 674
         |||||||||||||||| |||||||||| ||||||||||||||||||||||||||||||
Db   601 TGCGTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGGGGGTGAATTCCATGTGTAGCAG 660

Qy   675 TGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCCCCCTGGGTAACACT 734
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Db   661 TGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCCCCCTGGGTAACACT 720

Qy   735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 794
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 780

Qy   795 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCCTTGTAGCGCAGCTAACGCGTGA 854
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   781 CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCCTTGTAGCGCAGCTAACGCGTGA 840

Qy   855 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 914
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Db   841 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 900

Qy   915 GCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 974
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 960

Qy   975 GACATGTAGCGGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
         |||||||||||||||  | ||||||||  | |||||| ||||||||||||||||||||||||
Db   961 GACATGTAGCGGAATTTTCTAGAGATAGATTAGTGC-TTCGGGAACGCTAACACAGGTGCT 1019

Qy  1035 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1020 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1079

Qy  1095 CCTTGTCATTAATTGCCATCATCATTTAGTTGGGCACTTAATGAGACTGCCGGTGACAAACC 1154
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Db  1080 CCTTGTCATTAATTGCCATCATCATTTAGTTGGGCACTTAATGAGACTGCCGGTGACAAACC 1139

Qy  1155 GGAGGAAGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1214
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Db  1140 GGAGGAAGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1199

Qy  1215 ATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1274
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 ATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1259

Qy  1275 GTCGTAGTCCGGATTCGGGAGTCTGCGAACTCGACTCCGTGAAGTCGGAATGCTAGTAATCG 1334
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||  |||||||
Db  1260 GTCGTAGTCCGGATCGGGAGTCTGCGAACTCGACTCCGTGAAGTCGGAATCGTAGTAATCG 1319

Qy  1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1379

Qy  1395 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTGCCACGGCG 1453
         ||||||||||||||||||||||||| ||||||||||||||   | ||||| |||||||| |
Db  1380 TGGGAGTGGGTTTCACCAGAAGCAGTAGTCTAACCGTAAGTAAGGAGGGCGCTTGCCACGGTG 1439

Qy  1454 AGATTCATGACTGG 1467
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Db  1440 AGATTCATGACTGG 1453
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Query Match         92.6%;  Score 1358.8;  DB 7;  Length 1457;
Best Local Similarity  97.2%;  Pred. No. 0;
Matches 1414;  Conservative 0;  Mismatches 37;  Indels 3;  Gaps 3;

Qy    16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCACGGCACGGGTGCTTGCAC  75
         |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCGGCACGGGTGCTTGCAT  60

Qy    76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA 135
         |||||||||||||||||||||||||||||||||||||||||||
Db    61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGAACGGGAACGGGGGGTA 120

Qy   136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 195
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 180
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Qy 1275 GTCGTAGTCCGGATCGGAGTCTGCAACTGCTCCGTGAAGTCGGAATCGCTAGTAATCG 1334
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Db 1260 GTCGTAGTCCGGATCGGAGTCTGCAACTGCTCCGTGAAGTCGGAATCGCTAGTAATCG 1319

Qy 1335 CGGATCAGCATGTCGCGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
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Db 1320 CGGATCAGCATGTCGCGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1379

Qy 1395 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTTAACCGTAA-GAGGGCGTTTGCCACGGCG 1453
        |||||||||||||||||||||||||||||||||||||||| ||||| |||||||||||| 
Db 1380 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTTAACCGTAAGAGGAGGGGCTTGCCACGGTG 1439

Qy 1454 AGATTCATGACTCG 1467
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Db 1440 AGATTCATGACTCG 1453
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RESULT 13

US-10-659-948A-2

; Sequence 2, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA
US-10-659-948A-2

Query Match   92.5%;   Score 1357.2;   DB 7;   Length 1457;
Best Local Similarity   97.2%;   Pred. No. 0;
Matches 1413;   Conservative 0;   Mismatches 38;   Indels 3;   Gaps 3;

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Qy  16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCAGCGGCGGGTGCTTGCAC 75
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Db   1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCAGCGGATGCTTGCAT 60

Qy  76 CTGGTGCGGAGTGGGCGGACGGGTGAGTAATGCATCGGAACGTCCAGAAGTGGGGGATA 135
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 CTGGTGCGGAGTGGGCGGACGGGTGAGTAATGCATCGGAACGTCCAGAAGTGGGGGGTA 120

Qy 136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTACGGAGGAAAGCAGGGGATCGAAA 195
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ACGCATCGAAAGATGTGCTAATACCGCATATATACTCCTAAGGAGGAAAGCAGGGGATCGAAA 180

Qy 196 GACCTTGTCTTTGCTTTGGAGCGGCCGATGCCGGATTGACGGGGACCC 255
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GACCTTGTCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 240

Qy 256 CAAGGCAACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 315
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Db 241 CAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 300

Qy 316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1440 AGATTCATGACTGG 1453

RESULT 14
US-10-659-980A-2
; Sequence 2, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA
US-10-659-980A-2

  Query Match   92.5%; Score 1357.2; DB 7; Length 1457;
  Best Local Similarity   97.2%; Pred. No. 0;
  Matches 1413; Conservative   0; Mismatches   38; Indels   3; Gaps   3;

Qy   16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCAAGTCGAACGGCAGCGGGTGCTTGCAC 75
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Db   1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCAAGTCGAACGGCAGCGGGATGCTTGCAT 60

Qy   76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA 135
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAGAGGGGGGTA 120

Qy   136 ACGCATCGAAAGATGTGCTAATACCGGATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 195
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACGCATCGAAAGATGTGCTAATACCGGATATATCCTAAGGAGGAAAGCAGGGGATCGAAA 180

Qy   196 GACCTTGCTTTGGAGCGGCCGATGCGATGTCTGAGAGAGGCAGTGGGGAATTTGTGGTGGTAAAGGCCTAC 255
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GACCTTGCTTTGGAGCGGCCGATGCGATGTCTGAGAGAGGCAGTGGGGAATTTGTGGTGGTAAAGGCCTAC 240

Qy   256 CAAGGCAACGATCAGTAGTTGTCTGAGAGGACGACCAGCAGCCACACTGGGACTGAGACACG 315
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCAGCCACACTGGGACTGAGACACG 300

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTCGGACAATGGGCGCAAAGCCTGATC 375
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCGGACAATGGGCGCAAAGCCTGATC 360

Qy   376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAGA 434
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Db   361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAGA 420

Qy   435 AAAGGTTGTGACTAATAATCACAACTTATGATTGGTACCGACAGAAGAAGCACCGGCTAAC 494
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAAGGTTACGGTAAATAATCGTGACCCATGACGGTATCGACACAGAAGAAGCACCGGCTAAC 480

Qy   495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554
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Db   481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 540

Qy   555 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 614

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;   CURRENT FILING DATE: 2003-09-10
;   PRIOR APPLICATION NUMBER: US 09/573,684
;   PRIOR FILING DATE: 2000-05-19
;   PRIOR APPLICATION NUMBER: US 60/386,217
;   PRIOR FILING DATE: 2002-09-19
;   PRIOR APPLICATION NUMBER: US 60/386,218
;   PRIOR FILING DATE: 2002-09-19
;   PRIOR APPLICATION NUMBER: US 60/386,219
;   PRIOR FILING DATE: 2002-09-19
;   NUMBER OF SEQ ID NOS: 23
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 2
;   LENGTH: 1457
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA
US-10-659-983A-2

Query Match             92.5%;  Score 1357.2;  DB 7;  Length 1457;
Best Local Similarity   97.2%;  Pred. No. 0;
Matches  1413;  Conservative    0;  Mismatches   38;  Indels    3;  Gaps    3;
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Qy    16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTGCAC  75
         |||||||||||||||||||||||||||||||||||||||||||||||| ||| ||| ||
Db     1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGATGTGCTGCAT  60

Qy    76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTCCAGAAGTGGGGGATA 135
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Db    61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTCCAGAGAGAGGGGGTA 120

Qy   136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 195
         ||||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db   121 ACGCATCGAAAGATGTGCTAATACCGCATATCCTAAGGAGGAAAGCAGGGGATCGAAA 180

Qy   196 GACCTTGTGCTTTTGGAGCGGCCGATGCCGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
         |||||| || |||||||||||||||||| | ||||||||||||||||||||||||||||
Db   181 GACCTTGCGGTTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 240

Qy   256 CAAGGCAACGATCAGTTGGTCTGAGAGGACGAGCAGCCACACTGGGACTGAGACACG 315
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Db   241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 300

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
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Db   301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC 360

Qy   376 CAGCAATGCCGCGTGAGTGAAGAAG--CTTCGGGTTGTAAAGCTCTTTCAGTCGGAAGAA 434
         |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db   361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGGAAGAA 420

Qy   435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC 494
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Db   421 AAAGGTTACGGTGAAATAATCGTGACCCATGACGTATCGGAACAGACAGGAACACCGGCTAAC 480

Qy   495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATGATGAAATC 554
         ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db   481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 540

Qy   555 AAAGGGTGCGCAGGCGGCCTTGTAAGTCAGTGTGAAATCCCGGGGCTTAACCTGGGAAT 614
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Db   541 AAAGGGTGCGCAGGCGGCCTTGTAAGTCAGTGTGAAATCCCGGGGCTTAACCTGGGAAT 600

Qy   615 TGCGTTTGAAACTACACAAAGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 674
         |||||||||||| |||||| || ||||| ||||||||||| |||||||||||||||||||
Db   601 TGCGTTTGAAACTACACAAAGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 660

Qy   675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACT 734
         ||||||||||||||||||||||||| |||||||||||||||||||||| |||||||||||
Db   661 TGAAATGCGTAGAGATATGGAAGAACAGCCCCCTGGGTTAACACT 720

Qy   735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 794
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 780

Qy   795 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAGTCGCAGCTAACGCGTGA 854
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCTTGGTAACGAAGCTAACGCGTGA 840

Qy   855 AGTTGACCGCCTGGGAGTACGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 914
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   841 AGTTGACCGCCTGGGAGTACGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 900

Qy   915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTTT 974
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCCTT 960

Qy   975 GACGTAGTAGCCGAATATTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
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Db   961 GACATGTGAGCGAATTTTCTAGAGATAGATTAGTGC-TTCGGCAACGCTAACACAGGTGCT 1019

Qy  1035 GCATGGCTGTGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
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Qy  1095 CCTTGTCATTAGTTGCCATCATTTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1154
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Qy  1155 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1214
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Db  1140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1199

Qy  1215 ATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1274
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Qy  1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
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Db  1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1379

Qy  1395 TGGGAGTTGGGTTTCACCAGAAGTAGGGGCGTTAACCGTAA-GAGGGCGTTGCCACGGCG 1453
         |||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db  1380 TGGGAGTTGGGTTTCACCAGAAGTAGGGGCGTTAACCGTAACGGAGGGCGTTGCCACGGTG 1439

Qy  1454 AGATTCATGACTGG 1467
         ||||||||||||||
Db  1440 AGATTCATGACTGG 1453
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RESULT 15
US-10-659-983A-2

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; Sequence 2, Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
;   APPLICANT: Hovanec, Timothy A
;   TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
;   FILE REFERENCE: 81289-284779
;   CURRENT APPLICATION NUMBER: US/10/659,983A
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' Fri Apr 7 06:40:06 2006   us-10-659-983a-18.rnpbm

Db   721 GACGCTCATGCACGAAAGCGTGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 780

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Qy   855 AGTTGACCGCCTGGGGAGTACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGACCC 914
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
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Qy   915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 974
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Qy   975 GACATGTTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
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Qy   1215 ATACAATGGCGGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGCGC 1274
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Db   1380 TGGGAGTGGGTTTCACCAGAAGCAGGTAGTCTAACCCGTAACCCGTAAGGAGAGGGCGGCTTGCCCACGGTG 1439

Qy   1454 AGATTCATGACTGG 1467
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Db   1440 AGATTCATGACTGG 1453

Search completed: April 6, 2006, 20:33:50
Job time : 1289 secs

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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    April 6, 2006, 19:18:42 ; Search time 6253 Seconds
                                      (without alignments)
                                      10976.595 Million cell updates/sec

Title:        US-10-659-983A-18
Perfect score: 1467
Sequence:     1 ttgatcatggctcagatga.........acggcgagattcatgactgg 1467

Scoring table: IDENTITY_NUC
           Gapop 10.0 , Gapext 1.0

Searched:  41078325 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters:  82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     EST:*
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               2: gb_est2:*
               3: gb_est3:*
               4: gb_htc:*
               5: gb_est4:*
               6: gb_est5:*
               7: gb_est6:*
               8: gb_est7:*
               9: gb_gss1:*
              10: gb_gss2:*
              11: gb_gss3:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	802.6	54.7	6499	9	BH771024	LLMGtag74
	2	712.4	48.6	1954	8	CX109203	RECm0593
	3	650.4	44.3	941	7	CX296497	EST759211
	4	635	43.3	1084	9	BZ439740	BONDU54TF
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	6	625.2	42.6	1053	9	BZ447500	BONKF40TR
c	7	621.4	42.4	1010	9	BZ431523	BONHD88TF
c	8	616.6	42.0	1044	9	BZ463550	BONKC8CTF
c	9	616.6	41.9	1051	9	BZ494182	BONHR54TR
	10	614	41.9	889	7	CK280527	EST743249
c	11	613.8	41.8	1016	9	BZ426201	BOND228TF
	12	613.2	41.8	1079	9	BH705272	BOMKA47TF
c	13	612.6	41.8	1031	9	BH656222	BOMJZ86TF
c	14	611.6	41.7	1077	9	BZ450751	BONBQ63TR
	15	610	41.6	884	7	CK280528	EST743250
c	16	594.4	40.5	1054	9	BH647750	BOMND31TR
c	17	584	39.8	899	9	BZ685785	PUBDT54TD
	18	580.6	39.6	974	9	BZ440868	BONKT51TR
	19	579.4	39.5	951	9	BH651765	BOMFE30TR
c	20	571.8	39.0	756	8	DN469396	USDA-FP 1
	21	571.8	39.0	851	7	CK290947	EST753661
c	22	565.6	38.6	901	9	BZ461852	BONKO15TF
	23	564.4	38.5	787	7	CO159272	CO159272 FLD1_12 C
	24	562.4	38.3	918	9	B2437960	B2437960 BONNV72TF
	25	560.8	38.2	860	7	CN757363	CN757363 ID0AAA1CE
	26	560.2	38.2	977	9	B2459292	B2459292 BONKQ28TF
	27	559.2	38.1	746	9	AQ957362	AQ957362 LERAP36TF
c	28	556	37.9	1069	9	B2474941	B2474941 BONKR59TR
c	29	554.6	37.8	1106	9	B2469058	B2469058 BONHB54TF
	30	553.6	37.7	915	7	CV287759	CV287759 aof01-13m
	31	551	37.6	875	7	CV292617	CV292617 aof01-2ms
	32	550.8	37.5	947	7	B2464837	B2464837 BONKP76TR
c	33	545.6	37.2	716	9	AQ957363	AQ957363 LERAP36TR
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c	37	535	36.5	846	6	BH562180	BH562180 BOG2N83TF
	38	534.8	36.5	770	6	CF557211	CF557211 I115025D0
c	39	534.2	36.4	873	6	BH705306	BH705306 BOMIV08TF
c	40	533.2	36.3	875	9	BH547523	BH547523 BOGH290TF
	41	530.4	36.2	842	9	BH482629	BH482629 BOGNK19TR
	42	530.2	36.1	837	9	B2483676	B2483676 BOOAS16TR
	43	528.2	36.0	787	8	DN468747	DN468747 USDA-FP 1
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ALIGNMENTS

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RESULT 1
BH771024
LOCUS       BH771024            6499 bp    DNA     linear   GSS 01-MAY-2002
DEFINITION  LLMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
            subsp. cremoris genomic, genomic survey sequence.
ACCESSION   BH771024
VERSION     BH771024.1  GI:20373981
KEYWORDS    GSS.
SOURCE      Lactococcus lactis subsp. cremoris
  ORGANISM  Lactococcus lactis subsp. cremoris
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Lactococcus.
REFERENCE   1  (bases 1 to 6499)
  AUTHORS   Bolotin,A., Ehrlich,S.D. and Sorokin,A.
  TITLE     Studies of genomes of dairy bacteria Lactococcus lactis
  JOURNAL   Sci. Aliments (2002) In press
  COMMENT   Contact: Sorokin A
            Genetique Microbienne
            INRA
            CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
            Tel: 33 1 34 65 25 16
            Fax: 33 1 34 65 25 21
            Email: sorokine@jouy.inra.fr
            best homologue in strain IL1403 is ywgA (78%)
            Class: shotgun
            High quality sequence start: 30
            High quality sequence stop: 6471.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:1359"
                     /clone_lib="MG1363 Random Sequence Tag Library"
                     /note="Vector: pSGMU2; Site 1: SmaI; Library of
                     chromosomal fragments of L.lactis strain MG1363 was
                     prepared by partial AluI digestion or by sonication."
ORIGIN

Query Match             54.7%;  Score 802.6;  DB 9;  Length 6499;
Best Local Similarity   75.4%;  Pred. No. 3.5e-236;
Matches 1117;  Conservative   0;  Mismatches 349;  Indels 15;  Gaps 9;

Qy         1 TTGATCATGGCTCAGATTGAACCGCTGGGCGACGTGGGCGGCATGCTTTACACATGCAAGTCGAACGGC-A 59
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Db   1616  TGGGTTAAGTCCCGCAACGAGCGCAACCCCTATTGTTGAGTTGCCATCATTAAGTTGGGCA  1675
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Qy   1128  CTTTAATGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGATGACGTCAAGTCCTCATG   1187

Db   1676  CTCTAACGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGATGACGTCAAATCATCATG   1735
           |||||| ||||||||||||| ||||||||||||||||||||||||||||||||| ||||
Qy   1188  GCCCTTATGGGTAGGGCTCACACGTAATACATAGGCGGTACAGAGGGTTGCCAACCCG   1247

Db   1736  CCCCTTATGACCTGGGCTCACACGTGCTACAATGGGTCCGGATCGGAGTCTGCAACTCGACT  1795
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Qy   1248  CGAGGGGGAGCTAATCTCAGAAAGCGCGTCGTAGTCGGATCGGAGTCTGCAACTCGACT   1307

Db   1796  TGATGTTTAGCTAATCTCTTAAAACCATTCTCAGTTCGGATTGTAGGCTGCAACTCGCCT  1855
           ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy   1308  CCGTGAAGTCGGAATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGG   1367

Db   1856  ACATGAAGTCGGAATCGCTAGTAATCGCGGATCAGCACGCGCGGTGAATACGTTCCCGG   1915
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Qy   1368  GTCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTCACCAGAAGCAGATAGTCTA   1427

Db   1916  GCCTTGTACACACCGCCCGTCACACCGGGAGTGGGTTGGGAGTACCCGAGTGGTTGCCTA  1975
           |||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||
Qy   1428  ACCGTAA-GAGGGCGTTTGCCACGGCGAGATTCATGACTGG   1467

Db   1976  ACCGCAAGGAGGAGGGCGCTTCCTAAGTAAGACCGATGACTGG   2016
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RESULT 2

CX109203

LOCUS   CX109203   1954 bp   mRNA   linear   EST 03-JUN-2005

DEFINITION RECm0593 A normalized whole-life-cycle cDNA library of rice Oryza
            sativa (indica cultivar-group) cDNA clone EI051022, EI053J08,
            EI008B17, BI076L19, BI154A06, BI133B10, EI11 5', mRNA sequence.

ACCESSION   CX109203

VERSION   CX109203.1 GI:66922355

KEYWORDS   EST.

SOURCE   Oryza sativa (indica cultivar-group)

ORGANISM   Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.

REFERENCE   1 (bases 1 to 1954)

AUTHORS   Zhang,J., Feng,Q., Jin,C., Qiu,D., Zhang,L., Xie,K., Yuan,D.,
            Han,B., Zhang,Q. and Wang,S.

TITLE   Features of the expressed sequences revealed by a large-scale
            analysis of ESTs from a normalized cDNA library of the elite indica
            rice cultivar Minghui 63

JOURNAL   Plant J. 42 (5), 772-780 (2005)

PUBMED   15918889

COMMENT   Contact: Wang S
            National Key Laboratory of Crop Genetic Improvement
            Huazhong Agricultural University
            Wuhan 430070, China
            Tel: 86-27-87282044
            Fax: 86-27-87287092
            Email: shipingwang@hotmail.com
            Seq primer: T7.

FEATURES   Location/Qualifiers

     source   1..1954
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="mRNA"
                     /strain="indica"
                     /cultivar="Minghui 63"
                     /db_xref="taxon:39946"
                     /clone="EI051022, EI053J08, EI008B17, BI076L19, BI154A06,
                     BI133B10, EI11"
                     /tissue_type="whole plant"
                     /dev_stage="whole-life-cycle"
                     /lab_host="E. coli DH10B"
                     /clone_lib="A normalized whole-life-cycle cDNA library of
                     rice"
                     /note="Vector: pSPORT1; Site 1: SalI; Site_2: NotI; The
                     library is constructed based on the strategy of satuation

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Db    537  TTGATCCTGCTCAGGACGACGACCTGGCGCGCGTGCCTAATACATGCAAGTTGAGCGATGA   596
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Qy     60  GCACGGGTGCTTGCACCTGGTGGC-GAGTGGCGGACGGGTGAGTGAACGCGTGGGGAATCT   117

Db    597  AGATTGGTGTGTTGACCAATTTGAGAGAGCAGCGAACGGGTGAGTGAACGCGTGGGGAATCT   656
           ||||| |||| || |||||||||||||||||||||||||||||||||||||||||||||||
Qy    118  GTCCAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCT------   171

Db    657  GCCTTTGAGCGCGGGAGCAACATTTGGAAACGAAACCTTGTCGTTTGTGTTTGGAGCGGGCC   716
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Qy    172  -ACGGAGGAAAGCAGGGGATCGAAAGATCTTTGAAAGATGCCATCACTCAAAGATCAGATA   230

Db    717  ATAAGTTTTAAGTTTGGGGTAAAGGCCTACCAAGCAATCAGTAGTTGGTCTGAGAGGACGA   776
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Qy    231  GCTAGTTGGTGGGGTAAAGGCTCACCAAGGCGATCGATCATAGCCCACCTGAGAGGGTGA   290

Db    777  GCTAGTTGGTGGGGTAAAGGCTCACCAAGGCGATGATACATAGCCGACCTGAGAGGGTGA   836
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Db    837  TCGGGCACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTAGGGAATC   896
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Qy    351  TTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGC-TTCGGGT   409

Db    897  TTCGGCAATGACGAAGTCTGACCAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGAT   956
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Db    957  CGTAAAACTCTGTTGTTGGTAGAAGAAGAACGTTGGTGAGAGTCGAAAGCTCATCAAGTGACCG  1016
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Qy    469  TACCGCAGAAGAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGC   528

Db   1017  TAACTACCCCAGAAAGGGACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTCCC  1076
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Db   1077  GAGCGTTGTCCGGATTTATTGGGCGTAAAGCCAGCGCAGGTGGTTTATTAAGTCTGGTGT  1136
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Qy    589  GAAATCCCCGGGCTTAACCTGGGAATTGCCTTGAAAACTACAAAGCTAGAGTGTAGCAGA   648

Db   1137  AAAAGGCAGTGGCTCAACCATTGTA-TGCATTGGAAACTGGTAGACTTGAGTGGAGGAGA  1195
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Db   1196  GGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCCGTGG  1255
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Qy    709  CGAAGGCAGCCCCCTGGGTTAACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAG   768

Db   1256  CGAAAGCGGCTCTCTGGCCTGTAACTGACACTGAGGCTCGAAAGCGTGGGGAGCAAACAG  1315
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Qy    769  GATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTA   828

Db   1316  GATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGATGTGCTAGAGTGTAA   1375
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Db   1376  GTTCTCTGTATCGGCAGCTAACGCGTAACGCAATAAGCACTCCGCCTGGGGAGTACGGTT   1435
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Db   1436  GAAACTCAAAGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAA   1495
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Qy    948  GCAACGCCGAAAAACCTTACCTAGCTCTTGACATGTTAGCCGAATATTTGAGATAAATAGT  1007

Db   1496  GCAACGCGGAAGAACCTTACCAGGTCTTGACATACTCGTATTCCTAGAGATAGGAAGT   1555
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Db   1556  TCCTTCGGGACACCGGGGATACAGGTGGTGCATGGTCGTCGTCAGCTCGTGTCGTGAGATGT  1615
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Qy   1068  TGGGTTAAGTCCCGCAACGAGCGCAACCCCTGTCATTAATTGCCATCATTAGTTGGGCA   1127
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              hybridization with genomic DNA using rice cultivar Minghui
              63. This library consists of cDNA from 15 directionally
              cloned cDNA libraries constructed with different tissues
              from 9 developmental stages."

ORIGIN

Query Match    48.6%;  Score 712.4;  DB 8;  Length 1954;
Best Local Similarity   73.0%;  Pred. No. 2e-208;
Matches 1061;  Conservative   0;  Mismatches 336;  Indels  57;  Gaps   9;

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Qy   61  CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  120
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Db  173  GTGGTGTTT----------CCAGTGGCGAACGGGTGAGTAACGCGTAAGAACCTGCC  219

Qy  121  CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA  180
            || ||||||||||||||| ||  |||||| || ||||||||||||  ||||||||
Db  220  CTTGGAGGGGGAACAACAACTGGAAACGGTTGCTAATACCCCGTAGGCT----------  268

Qy  181  AGCAGGGGATCGAAAGCACCTTGTGCTTTTGGAGCGGCCGATGGCCTGATTAGCTAGTTGGT  240
            ||| | |||||||||||||||  ||||||||||||||||||||||||||||||||| |||
Db  269  --GAGGAGCAAAAGGAGAAAT CCGCCCAAGGAGGGGGGGTCGCGTCGATTAGTTAGTTGGT  326

Qy  241  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTCGTCTGAGAGACGACCAGCCACAC  300
            |||||||||||||||||||||||||||| | ||||||||||||||| |||| ||||||||
Db  327  GAGGGAATAGTTACCAAGGCGATGATCAGTAGTCAGTCCGAGAGGATGATCAGCCACAC  386

Qy  301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  387  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATG  446

Qy  361  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTC  419
            ||||||| |||| |||||||||||||||||| | ||| || | | ||||||||||||
Db  447  GGCGAAAGCCTGACGGAGCAATGCCGCGTGGAGTGAAGAAGGTCGGCGGTTGTCAACTTC  506

Qy  420  TTTCAGTCGGAAGAAAAGGTTGTGACTAATAATCACAACTTATGATGATGTACCGACAGAA  479
            |||||| | |||||||||
Db  507  TTTTCTCCGGAAGAAGAA----------CAATGACGGTATCTGAGGAA  543

Qy  480  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  539
            |||||||||||| | | |||||||||||||||||||||||| ||||||||||||||
Db  544  TAAGCATCGGCTAACTTCTGTCCAGCAGCCGCGGTAAGACGGATGCAAGCGTTATCC  603

Qy  540  GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCCGTTTGTGAAGTCAGATGTGAAATCCCCGG  599
            |||| | | |||||||||||||| | |||||||| | | |||||| || |||||||| |||
Db  604  GGAATGATTGGGCGTAAAGCGTCTGTAGGTGGCTTTTCAAGTCCGCCGTCAAATCCCCAGG  663

Qy  600  GCTTAACCTGGGAATTGCCGTTGAAACTACAAAGCTAGAGTGTAGGAGAGGGGGTGGAA  659
            |||||||||||| |||||||||||||| | |||||| ||||||||||| |||||||||||
Db  664  GCTCAACCCTGGACAGGGCGGTGAAAACTACCAACTGGAGTACGGTAGGGGCAGAGGGAA  723

Qy  660  TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCC  719
            |||||| | | | ||||||||||||||| | |||||| | |||| |||||||||||||||
Db  724  TTTCCGGTGGAGCGGTGAAATGCGTAGATATCGGGGAAGAACACCAGTGGCGAAGGCGGCTC  783

Qy  720  CCCTGGGTTAACACTGACGCTCATGCGACGAAAGCGTGGGGAGCGCAAACAGGATTAGATACC  779
            ||| ||||| ||| || | ||| ||| || || | | ||||| | ||||| ||||||||||
Db  784  TGCTGGGCCGACACTGACACTGAGGAGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC  843

Qy  780  CTGG--TAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTG--G  835
            ||||   |||||  | | ||||||||| | | | ||| |||||| | || ||||| |
Db  844  CCAGATAATCCATAGCCGTAAACGATGGATACTAGGTGCTGCTGCGGATTTGTGACTCGCAG  903

Qy  836  TAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA  895
            | ||||||||| || || |||| || ||| |||||| |||| || |||||| |||| |||
Db  904  TGCTGTAGGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGGTCGCAAGAATGAAACTCA  963

Qy  896  AAGGAATTGACGGGGACCCCGCACAAGCGGTGGAGCATGTGGATTAATTCGATGCAACGCG  955
            ||||||||||| || || || ||||||| || ||||||| |||||| |||||||| |||||
Db  964  AAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAAGCG  1023

Qy  956  AAAAACCTTACCTACCCTTGACATGTAGCGGAATATTTTAGAGATAAAATAGTGCCTTCGG  1015
            ||||||||||||||||  ||||||||||| |||| |||  ||| || || ||||||| ||
Db 1024  AAGAACCTTACCAGGGCTTGACATGCCCGGAATCCTCTTGGAAGAGAGGGGTGCCCTTCGG  1083

Qy 1016  GAACGCTAACACAGGTGCTGCATGGCTGTCGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA  1075
            ||||| ||| ||||||||| ||||| |||||||||||||||||||| || |||| | |||
Db 1084  GAACGCGGACACAGGTGTGTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA  1143

Qy 1076  GTCCCGCAAGCGAGCGCAACCCTGTCATTAATTGCCATCATTAGTTGGGCACTTAATG  1135
            ||||| |||||||||||||||||||  || ||||| | | ||||||||||||||||||
Db 1144  GTCTCGCAACGAGCGCAACCCTCGTGTTTAGTTGCCA-CTATGAGTTTGGGTTGTTCCA-  1202

Qy 1136  AGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTAT  1195
            ||||||| |||||||||| ||| ||| | |||||||| || | || ||||||| || ||
Db 1203  AGACCGCCGGTGTTAAGCCGGAGGAAGGAGGGGATGACGTCAAGTCATCATGGCCCTTAT  1262

Qy 1196  GGGTAGGGCTTCACACTGTAATACAACATGCTGCCAACCCGCAGGGTGCCAACCCCGGAGGGGG  1255
            ||| || ||| | |||| | ||| || ||||| |||||||||||||| | || || || |||
Db 1263  GCCCTGGGCGACACACGTGCTACAATGGCGGGGACAAAGGGCTGCGATCTCGCGAGGGTG  1322

Qy 1256  AGTAATCTCAGAAAGGCCGTCGTAGTCCGATCGGATCGGTCTCGACTCGTGAAG  1315
            ||||||||| |||||||||| || ||||||||||  || ||||||||| || |||||
Db 1323  AGTAACTCCAAAAACCCGTCCTCAGTTCGGATTCGGAGGCTGCAACTCGCCTCTCATGAAG  1382

Qy 1316  TCGGAATCGCTAGTAATCGCGGATCAG-CATGTCGCGGTGAATACGTTCCCGGTCTTGT  1374
            |||||||| || ||||||||||||| | | ||| | |||||||||||||||| |||||
Db 1383  CAGGAATCGCTAGTAATCGCCGGTCAGCATCACGGCGGTGAATACGTTCCCGGGCCTTGT  1442

Qy 1375  ACACACCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTC-TAACCGTA  1433
            |||||||| | ||||||||||| ||||| |||||| |||| |||||| | ||||||||
Db 1443  ACACACCGCCCGTCACACTATGGGAGCTGGCCATGTTTGAAGTCATTACCTTAACCGTA  1502

Qy 1434  AGAGGGCTTTGCC  1447
            || ||| | |||
Db 1503  AGGAGGGGGATGCC  1516
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RESULT 3
CK296497
LOCUS        CK296497                         941 bp    mRNA        linear    EST 02-AUG-2004
DEFINITION   EST759211 Nicotiana benthamiana mixed tissue cDNA library,
             normalized, full-length Nicotiana benthamiana cDNA clone NBMD226 5'
             end, mRNA sequence.
ACCESSION    CK296497
VERSION      CK296497.1  GI:39881943
KEYWORDS     EST.
SOURCE       Nicotiana benthamiana
ORGANISM     Nicotiana benthamiana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
             asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE    1  (bases 1 to 941)
AUTHORS      Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
             Staskawicz,B., Jin,H. and Baker,B.
TITLE        Generation of EST sequences from Nicotiana benthamiana
JOURNAL      Unpublished (2003)
COMMENT      Contact: Robin Buell
             The Institute for Genomic Research
             9712 Medical Center Dr, Rockville, MD 20850, USA
             Email: potato-array@tigr.org
             Clones can be requested from the University of Arizona Genomics
             Institute via http://genome.arizona.edu/orders/ .
             Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES             Location/Qualifiers
     source          1..941
                     /organism="Nicotiana benthamiana"
                     /mol_type="mRNA"
                     /db_xref="taxon:4100"
                     /clone="NBMD226"
                     /tissue_type="abiotic and biotic stress-treated leaves,
                     callus tissue and root tissue"
                     /lab_host="DH10B-TonA"
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Db   783  CTGGTAGTCCACGCGCCTAAACGATGTCAACTAGCCGTTGGG-AGCCTTGAGCTCTTAGTG  841
                ||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Qy   840  GTAGCTAACGCGTGAAGTTGACCGGCTGGGGAGTACGGTCGCAGGATTAAAACTCAAAGG  899

Db   842  GCAGCTAACGCATTAGTTGACCGGCTGGGGAGTACGGCCCCAGGTTAAAACTCAAATG    901

Qy   900  AATTGACGGGGACCCGCACAAGCGGTGGGATTATGTGGATT  939
                |||||||||||||||||||||||||||||||||||||
Db   902  AATTGACGGGGACCCGCACAAGCGGTGGGAGCATGTGGTTT  941
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RESULT 4

LOCUS   BZ439740   1084 bp   DNA   linear   GSS 13-DEC-2002
DEFINITION   BZ439740 BONDU54TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONDU54,
                genomic survey sequence.
ACCESSION   BZ439740
VERSION   BZ439740.1 GI:26695676
KEYWORDS   GSS.
SOURCE   Brassica oleracea
  ORGANISM   Brassica oleracea
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 1084)
  AUTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
                Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
  TITLE   Whole genome shotgun sequencing of Brassica oleracea and its
                application to gene discovery and annotation in Arabidopsis
  JOURNAL   Genome Res. 15 (4), 487-495 (2005)
  PUBMED   15805490
COMMENT   Other_GSSs: BONDU54TR
                Contact: Chris Town
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA.
                Tel: 301-838-3523
                Fax: 301-838-0208
                Email: cdtown@tigr.org
                DNA is from a doubled haploid provided by Tom Osborn.
                Seq primer: TF
                Class: sheared ends.
FEATURES   Location/Qualifiers
     source   1..1084
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH1"
                     /db_xref="taxon:3712"
                     /clone="BONDU54"
                     /clone_lib="BO_1.6_2_KB_tot"
                     /note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared
                     total DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

Query Match   43.3%; Score 635; DB 9; Length 1084;
Best Local Similarity   76.9%; Pred. No. 1.6e-184;
Matches 837; Conservative   0; Mismatches 225; Indels 27; Gaps 4;

Qy   252 CTACCAAGGCAACGATCAGTAGTTGGCTCTGAGAGGACGACCAGCCACACTGGGACTCGAGA 311
               ||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   3 CTTACCAGGCCCAGCGATGATCAGTAGTCGTGGTCGTCCGGAGAGA-GATCAGCCACACTGGGACTCGAGA   61

Qy   312 CACGGGTCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 371
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 CACGGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCT 121

Qy   372 GATCCAGCAATGCCGCGTGAGTGAGGAAGG-CTTCGGCGTTGTAAAGCTCTTTCAGTCGAG 430
               |||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   122 GACGAGCAATGCCGCGTGCGGGTAGAAGGGCTGCCGCCTACGGGTCCTGAAGTCTTTTCCCAGAG 181

Qy   431 AAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGC 490
               ||| ||||||||||||
Db   182 AAG--AAGCAATGACGGTATCTCGGGAATAAGCATCGGC 218
```

REFERENCE
AUTHORS
TITLE

JOURNAL
PUBMED
COMMENT

clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1143)
Cheng,Y.M. and Lin,B.Y.
Cloning and characterization of maize B chromosome sequences
derived from microdissection
Genetics 164 (1), 299-310 (2003)
12750341
Contact: Bor-yaw Lin
Department of Molecular Biology
National Chung Hsing University
250 Kuo Kuang Rd, Taichung 402, Taiwan (ROC)
Tel: 886-4-2285-1885
Fax: 886-4-2287-4879
Email: bylin@dragon.nchu.edu.tw
Insert Length: 1143    Std Error: 0.00
Class: PCR fragment.

FEATURES        Location/Qualifiers
source          1..1143
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /cultivar="L289"
                /db_xref="taxon:4577"
                /clone="pBPC15"
                /sex="hermaphrodite"
                /cell_type="Pollen mother cells"
                /dev_stage="Meiosis I"
                /lab_host="DH5alpha"
                /clone_lib="Maize B chromosome PCR DNA library"
                /note="Vector: pBSK-; The library was constructed from
                microdissected B chromosome DNA."

ORIGIN

Query Match          43.0%;   Score 631.2;   DB 9;   Length 1143;
Best Local Similarity  89.3%;   Pred. No. 2.4e-183;
Matches 738;   Conservative 0;   Mismatches 78;   Indels 10;   Gaps 5;

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Qy   491 TAACTACGTGCCAGCAGCGCGCGTAATACGTAGGGTGCGAAGCGTTAATCGGAATTACTGG 550
         |||||  ||||||||||||||  ||||||||    ||  ||||||||| | ||||| | ||
Db   219 TAACTCTGTGCCAGCAGCCGCCGCGTAATACAGAGATCGCAAGCGTTATCCGGAATGATTGG 278

Qy   551 GCGTAAAGGGTGCGCAGGCGGCTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGG 610
         | ||||||| | | | |||||||| |||||| | | |||||||| | ||||| |||| || 
Db   279 GGGTAAAGCGTCGTGTAGTGGCTTTTAAGTCCGCCGTCAAATCCCAAGGGCTCAACCCTG 338

Qy   611 GAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAATTCCATGTGTA 670
         ||   |||| ||||||||  |||||  |||   | |||||||  |||||||||| || | 
Db   339 GACAGGCGGTGAAACTAACCAGCTTGAGTACGGTAGGGGCAGAGGGAATTTCCGGTGGA 398

Qy   671 GCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGCGAAGGCAGCCCCTGGGGTAA 730
         || |||||||||||||||||  | ||| ||  |  | |||| | |   |||| |  |||
Db   399 GCGGTGAAATGCGTAGAGATCGGAAATGCGAAAGAACACCACCAACGACGAAGCACTCTGCTGGGCCGA 458

Qy   731 CACTGACGGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA 790
         |||||||  | | |  |||||||| ||||||||||| ||||||||||||| |||||||||| 
Db   459 CACTGACACTGAGAGACGAAAGCTAGGGGAGCAAATGGCGAATGGATTAGATACCCCAGTAGTCCT 518

Qy   791 CGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTG--GTAACGTAGCTAAC 848
         |||| |||||||||| | |||||| ||  |  |  |  | |  |||||||| 
Db   519 AGCCGTAAACGATGATACTAGGCGCTGTGCCGTATCGACCCGTGCAGTGTGTGTAGCTAAC 578

Qy   849 GCGTGAAGTTGACCGCCTGGGAAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGG 908
         |||| |||| | |||||||||| ||||  |||||||| |  | |||||||||||||||||| 
Db   579 GCGTTAAGTATCCCGCCTGGGAGTACTTCCGCAAGAGTAACCTTCCCAAGAATGAAACTCAAAGGAATTGACGG 638

Qy   909 GGACCCGCACAAGCGGTGGATTATGGGATTAATTCGATGTTGTTTAATTCGAAGCAACGCGAAAAACCTTACCA 968
         || |||||||||||||||||    | |  |||| | || |||||| ||||||||||||||||  | ||||||| 
Db   639 GGGCCCGCACAAGCGGTGGAGCAGGTGTTGTTTAATTCGAAGCAACGCGAAGAGCGAACCTTACCA 698

Qy   969 ACCCTTGACATGCTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACA 1028
         | ||| || ||||  |||||| |  | | | | | |     |||||||||||| | |||| 
Db   699 GGGCTTGACATGCCATGCGAATGTCGTTGCGTCGTCGTCCGTCGTGTCGTAAGGGTGTTCCTCGGGAACGCGGACACA 758

Qy  1029 GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG 1088
         ||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   759 GGTGTCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG 818

Qy  1089 CGCAACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGA 1148
         ||||||||| || ||| |||||||| |||| ||||||||| |  ||| ||||||||||| 
Db   819 CGCAACCCTCGTGTTTTAGTTGCCAGCATTCAGTTGGGCACTCTGACACTGCCGGTGA 878

Qy  1149 CAAACCCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGCCCTTATGGGTAGGGGCTTCA 1208
         |||  ||||||||||||| |||||||||||||| |||||  |||||||  ||||||| || 
Db   879 TAAGCCGGAGGAAGGTGAGGATGACGTCAAGTCAAGTCCTCAAGTCCCTTATGCCCTGGGGGACA 938

Qy  1209 CACGTAATACAAATGGCCGTACAGAGGGTCGCCGTAATCTTCAGA 1268
         |||||  |||| ||||||| ||||| ||||||| | | || ||| 
Db   939 CACGTGCTACAATGGCCGGTACAAAGGGTCGCGGATCTCGAGTCGAGCTGAGCGTGAGCGTCAACTCCAAA 998

Qy  1269 AAGCGCCTCGTAGTCCGGATCGGATGCTCGCAACTCGCCTGCGTGAAGTCGGAATCGCTAG 1328
         ||  | | |  | |||||| |||| | |||||||||||||||| |||  |||| |||||||
Db   999 AACCCGTCCCTCAGTCGGATTGCCAGCGTGCAACTCGCCTGCGCAACTCGCTAG 1058

Qy  1329 TAATCGCGG 1337
         |||||||  
Db  1059 TAATCGCCG 1067
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Qy   645 CAGAGGGGGTGGAATTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCG 704
         ||||||||||  ||||||| |||||||||||||||||||||||||||| || ||||| | 
Db  1143 CAGAGGGGGTAGAATTCCACGTGTAGCAGTGAAATGCGTAGAGATATGTGAGGAACACCG 1084

Qy   705 ATGGCGAAGGCAGCCCCTGGGTTAAACTACGACGCTCATGCACGAAAGCGTGGGGAGCAA 764
         ||||||||||||||||| |||| |||  | |||| || |  ||| | ||| ||||||||| 
Db  1083 ATGGCGAAGGCAGCCCCCTGGGTCAAGATTGACGCTCAAGATTGACGCTCAAGATTGACGCCGTGGGGAGCAA 1024

Qy   765 ACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCTT 824
         |||||||||||||||||||||||||||||||||||||||||| |||||||| | ||||| 
Db  1023 ACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCTACTAGTTGTCGGGTCTT 964

Qy   825 ACTAGGCTTGGTAACGTAGCTAACGGTGAAGTTGACCGCCTGGGAAGTGACGTCGCAGG 884
         | |  | ||| |||||||| |||||||||||| |||| || ||||||||||| | | || 
Db   963 AATTGACGTTGAACGTAACGGTGAAGTAGACCCCTCGGGAGTGACGTACGCGCAAG 904

Qy   885 ATTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTATGGGATTAATTC 944
         ||||||||||||||||||||||||||||||||||||||||||| |  ||||||||||| 
Db   903 ATTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTGATGGGATTAATTC 844

Qy   945 GATGCAACGCGAAAAACCTTACCTACCCTTGACACATGTAGCGAATATTTTAGAGATAAAAT 1004
         ||||||||||||||||||||||||||||||||||    | |||||| |          | 
Db   843 GATGCAACGCGAAAAACCTTACCTACCCTTGACATGCTGCGAATCCTTGACACGTCGTGTGA 784

Qy  1005 AGTG--CCTTCGGGAACGTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGA 1062
         ||||   |   | ||||| ||||||||||||||||||||||||||||||||||||||||
Db   783 AGTGCTCGAAAGAGAACCAGTACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGA 724

Qy  1063 GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTAGTT 1122
         |||||| | ||||||||||||||||||||||||||||||||| ||||||  |  | ||   
Db   723 GATGTT-GTTAAGTCCCGCAACGAGCGCAACCCTTGTCATTAGTTGCTACGAA----- 670

Qy  1123 GGGCACTTTAATGAGACTGCCGGTGACAAACCGGAAGTGGGGATGACGTCAAGTCC 1182
         ||||||| |||||| ||||||||||||| ||||||| |||||| ||||||||||| 
Db   669 GGGCACTCTAATGAGACTGCCGGTGACAAAACCGGAAGGTGGGGAT-ACGTCAAGTCC 611

Qy  1183 TCATGGCCCTTATGGTAGGGGCTTCACACGTAATACAATGGGCGCGTACAGAGGGTTGCCA 1242
```

RESULT 5
BH814966/c
LOCUS   BH814966   1143 bp   DNA   linear   GSS 31-MAY-2003
DEFINITION pBPC15 Maize B chromosome PCR DNA library zea mays genomic clone
            pBPC15, genomic survey sequence.
ACCESSION   BH814966
VERSION   BH814966.1 GI:31249923
KEYWORDS   GSS.
SOURCE   Zea mays
  ORGANISM Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Qy   335 GCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTG 394
           ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   932 GCAGCAGTGGGGAATTTCCG-CAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGGAGG 874

Qy   395 AAGAAGG--CTTCGGGTTGTAAAGCTCTTTCAGTCAGAGAAGAAAAAGGTTGTGACTAATAAT 453
           |||||| |||||||||||||||||||| |||| |||
Db   873 TAGAAGGCCTTACGCGTTGGGGAACTTCTTTTTCCCAGAGAAG------------------- 834

Qy   454 CACAACTTATGATGCCAGCAGAGAGCACCGGCTAACTACGTGCCAGCAGCCGCGG 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   833 ---AAGCAATGACGGTATCTGGGAATAAGCATCGGCTAACTCGTGCCAGCAGCCGCGG 777

Qy   514 TAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCT 573
           ||||||||||||||||||||| ||||||||||| ||||||||| ||||||||
Db   776 TAATACAGAGGGTGCAAGCGTTATCCGGAATTACTGGGCGTAAAGGGTCTGTAGGTGGCT 717

Qy   574 TTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAATTGCGTTTGAAAACTACAAAG 633
           ||| |||||||||||||||||||| |||||||||| |||||||||||||||||||||||
Db   716 TTTTAAGTCCGCCGTCAAATCCCGACGGGCTCAACCCTGGACAGGCGGTGGAAACTACCAAG 657

Qy   634 CTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAGTGAAATGCGTAGAGATATG 693
           |||||||| | || |||||||||||||||||||||| |||||||||||||||||||||||
Db   656 CTTGAGTACGTAGGGGGGCAGAGGAATTTCCGGTGGAGCGGTGAAATGCGTAGAGATCGG 597

Qy   694 GAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACTGACGCTCATGCACGAAAGC 753
           ||| ||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   596 AAAGAACACCAACGGCGAAAGCACTCTGCTGGGCCCACACTGACGCTGAGAGACGAAAGC 537

Qy   754 GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGT 813
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   536 TAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAAACGGTGAAACGATGATACTAGG 477

Qy   814 TGTTGGGCCTTACTAGGCTTG--GTAACGTAGTAACGCGGTGAATGGCTAACGCCCTGGGGA 871
           |||||| ||| |||||||||| || ||||||||||| |||||||
Db   476 CGCTGTGCGTATCGACCCGTGCCAGTGCTGTGAGTGCTAACGTCCCTGCGGGGA 417

Qy   872 GTACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGGACCCGCACAAGCGGTGGATTA 931
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Db   416 GTACGGTCGCAAGAATGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCA 357

Qy   932 TGTGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCCTGACATGTAGCGAATATT 991
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Db   356 TGTGGTTTAATTCGATGCAAAGCGAAGAACCTTACCAGGGCTTGACATGCCGGCTGTCGTCAGC 297

Qy   992 TTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCTGCTGCGTGTCGTCAGC 1051
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Db   296 CTTGAAAGAGAGGGTGCCTTCGGGAACGCGGACAGTGTGATAAGTCCGGTCGTCAGC 237

Qy   1052 TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACCCTTGTCATTAATAGTTTAGTTGCC 1111
           |||||||||||||||| |||||||||| ||||||||||||| ||||||||||
Db   236 TCGTGCCGTAAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTGTTTAGTTGCC 177

Qy   1112 ATCATTTAGTTGGGACTTTAATGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATG 1171
           ||||| |||||||||| |||||| |||| ||||| |||||||||||||||||||||
Db   176 ACCGTTGAGTTGGACCCTGACACTGCGGTGATGATAAGTCGGAGGAAGGTGAGGATG 117

Qy   1172 ACGTCAAGTCCTCATGGCCCTTATGGTGAGTAGGCTTCACACGTAATACAATGGCCGGTACA 1231
           ||||| ||||||||||||||||| || |||||| ||||||||| ||||||||||||||
Db   116 ACGTCAAGTCATCATCATGCCCCTTATGCCCTGGGCGACACACGTGCTACAATGGCCGGGACA 57

Qy   1232 GAGGGTTGCCAACCCCGAGGGGGAGCTAATCTCAGAAAGGCCGGTCGTAGTCCGGA 1287
           |||||| ||||||||||||||||||||||||||||||||||| |||||||||||||
Db   56   AAGGGTTCGGATCCAGAGAGGGTGAGCTAACTCCAAAAACCCGGTCCTCCAGTTCGGA 1

Db   610 TCATGCCCCTTATGGGTAGGGCCTTCACACGTCATCACGTGTACATACAGAGCCGCGCCA 551
           ||||||||||||||||||||||||||||||| | ||||||
Qy   1243 ACCCCGAGGGGGGAGCTAATCTCAGAAAGGCCGTCGTAGTCCGGATCGGTCGTCTGCAACT 1302
           ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   550 ACCCGAGGGGGGAGCTAATCGTAGCAGAAAGTGTATCGTAGTCGTAGTAATCGTGCCAACT 491

Qy   1303 CGACTCCGTGAAGTCGGAATCGTCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTT 1362
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   490 CGACTGCGATGAAGTTGGAATCGTCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTT 431

Qy   1363 CCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTTGGGTTTCACCGAAGCCAGATA 1422
           ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   430 CCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGCCGGGTTTTACCGAAGTAGGTA 371

Qy   1423 GTCTAACCGTAA-GAGGGCGTTGCCACGCGGGCGAGATTCATGACTGG 1467
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Db   370 GCTTAACCGCACAAGGGGGCGCCTTACCACGTGGATTCGTGACTGG 325

RESULT 6
BZ447500/c
LOCUS   BZ447500   1053 bp   DNA   linear   GSS 13-DEC-2002
DEFINITION   BONKF40TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONKF40,
             genomic survey sequence.
ACCESSION   BZ447500
VERSION   BZ447500.1 GI:26712943
KEYWORDS   GSS.
SOURCE   Brassica oleracea
  ORGANISM   Brassica oleracea
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
             rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 1053)
  AUTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
             Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
  TITLE   Whole genome shotgun sequencing of Brassica oleracea and its
             application to gene discovery and annotation in Arabidopsis
  JOURNAL   Genome Res. 15 (4), 487-495 (2005)
   PUBMED   15805490
COMMENT   Other_GSSs: BONKF40TF
             Contact: Chris Town
             TIGR
             9712 Medical Center Drive, Rockville, MD 20850, USA.
             Tel: 301-838-3523
             Fax: 301-838-0208
             Email: cdtown@tigr.org
             DNA is from a doubled haploid provided by Tom Osborn.
             Seq primer: TR
             Class: sheared ends.
FEATURES   Location/Qualifiers
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                     total DNA inserted into pHOS1 using BstXI linkers"
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Best Local Similarity   76.8%; Pred. No. 1.7e-181;
Matches 826; Conservative   0; Mismatches 223; Indels 27; Gaps   4;

Qy   215 GGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAGGCAACGATCAGTAGT 274
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Db   1052 GGCTCGCCTCGATTAGCTAGTTGGTGGGGTAAGGCCTAATAGCTTACCAAGGCGATGATCAGTAGC 993

Qy   275 TGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG 334
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Db   992 TGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG 933

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KEYWORDS   GSS.
SOURCE     Brassica oleracea
ORGANISM   Brassica oleracea
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 1010)
AUTHORS    Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
           Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE      Whole genome shotgun sequencing of Brassica oleracea and its
           application to gene discovery and annotation in Arabidopsis
JOURNAL    Genome Res. 15 (4), 487-495 (2005)
PUBMED     15805490
COMMENT    Other_GSSs: BONHD88TR
           Contact: Chris Town
           TIGR
           9712 Medical Center Drive, Rockville, MD 20850, USA.
           Tel: 301-838-3523
           Fax: 301-838-0208
           Email: cdtown@tigr.org
           DNA is from a doubled haploid provided by Tom Osborn.
           Seq primer: TF
           Class: sheared ends.
FEATURES   Location/Qualifiers
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           total DNA inserted into pHOS1 using BstXI linkers"
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Query Match             42.4%;  Score 621.4;  DB 9;  Length 1010;
Best Local Similarity   77.5%;  Pred. No. 2.5e-180;
Matches  801;  Conservative  0;  Mismatches  206;  Indels  26;  Gaps  3;

Qy   226 GATTAGCTAGTTGGTGGGGTAAAGGCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAG 285
          ||||||||||| ||||| |||||||||||||| |||||||||||||| ||||||||
Db  1010 GATTAGCTAGTGGGGTGAGGCAATAGTTACCAAGGCAATAGTTCAGTAGCTGGTCCGAGAG 951

Qy   286 GACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGG 345
          || || ||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   950 GATGATCAGCCACACTGGGACTGAGACACGGCCCCAGACTCCTACGGGAGGCAGCAGTGGG 891

Qy   346 GAATTTTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCCGTGAGTGAGTGAAGAAG-CTT 404
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Db   890 GAATTTTCCCGAATGGGCGAAAGCCTGACGGGAGCAATGCCGCGTGAGTGAAGAAGGCCTA 831

Qy   405 CGGGTGTAAAGCTCTTCAGTGCAGAAGAGAAAAGGTTGTGACTAATAATCCAACTTATG 464
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Db   830 CGGGTCCTGAACTTCTTTTCCCAGAGAAG-----------------AAGCAATG 794

Qy   465 ATGGTACCGACAGAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGG 524
          ||||| |||| || ||||| |||||||||| |||| |||||||||||||||||| ||||
Db   793 ACGGTATCTGGGAATAAGCATCGGCTAACTCTGTCCAGCAGCCGCGGTAATACAGAGG 734

Qy   525 GTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCCGCTTTGTAAGTCAG 584
          ||||||||||||| ||||||| |||||||||||| ||| ||||||| |||||||||||||
Db   733 ATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCGTAGGCGGCTTTTTAAGTCCG 674

Qy   585 ATGTGAAATCCCCGGGCTTAACCTGGAATTGCGTTGAAACTACAAAGCTAGAGTGTAG 644
          |||  ||||| ||||| ||||| ||||   |||| ||||||||| |||| |||| |||
Db   673 CCGTCAAATCCCAGGGCTCAACCCTGGACAGGCGGCGGTGAAACTACCAAGCTTGAGTACGG 614

Qy   645 CAGAGGGGGGTGGAATTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCG 704
          |||||||  |||||||||| | |||||||||||||||||||||||   |||||| ||| |
Db   613 TAGGGGCAGAGGGAATTCCGGTGGAGCGGTGAAATGCGTAGAGATCGGAAGAAGAACACCA 554

Qy   705 ATGGCGAAGGCAGCCCCCTGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAA 764
          |||||| ||| ||||||  |||||
Db   553 ACGGCGGAAGCACTCTCTGGTCCTGGCCGCGACACTGACGCCTAAACGATGTCAACTAGTTGTTGGGCGAGCGA 494

Qy   765 ACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTT 824
          | ||||||||||||||| |||||||| |||||||||||||
Db   493 ATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATTACTAGGCGCTGTGCGTA 434

Qy   825 ACTAGGCTTG--GTAACGTAGCTAACGGTGAAGTTGACCGCCTGGGGAGTACGTCGCA 882
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Db   433 TCGACCCGTGCAGTGCGTGTAGCTAACGGTTAAGTATCCCGCCTGGGGAGTACGTCCGCA 374

Qy   883 GGATTAAAACTCAAAGGAATTGACAGGGACCCGCACAAGCGGTGGATTATGTGGATTAAT 942
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Db   373 AGAATGAAACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAAT 314

Qy   943 TCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGTAGGCAATATTTTAGAGATAAA 1002
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Db   313 TCGATGCAAAGCGAAGAACCTTACCAGGGCTTGACATGCCGTGTCGTCAGCTGCGTCGTGA 254

Qy  1003 ATAGTGCCTTCGGAACGCTAACACAGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGA 1062
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Db   253 GGGGGTGCCTTCGGGAACGCGACACAGTGTGCATGGCTGTCGTCAGCTCGTGTCGTGCCGTAA 194

Qy  1063 GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTTAGTT 1122
          |||||||||||||||||||||||||||||||||||  |||| |||||||| || ||||||
Db   193 GGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTGTTTAGTTGCCACCGGTGAGTT 134

Qy  1123 GGGCACTTTAATGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCC 1182
          |||  ||| |||| |||||||||||| || |||||||||||||||||||||||||||||
Db   133 TGGAACCCTGAACAGACTGCCGGTGATAAGCCGGAGGAAGGTGGGGATGACGTCAAGTCA 74

Qy  1183 TCATGGCCCTTATGGGTAGGGCTTCACACGTAATACAATGGCCGTACAGAGGGTTGCCA 1242
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Db    73 TCATGCCCCTTATGCCCGTGGGCACACATCGTACAATGGCCGGACAAAGGGTCCGGA 14

Qy  1243 ACCCGCGAGGGGG 1255
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Db    13 TCCCGCGAGGGTG 1


RESULT 8
BZ463550/c
LOCUS       BZ463550              1044 bp    DNA     linear   GSS 13-DEC-2002
DEFINITION  BONKC86TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONKC86,
            genomic survey sequence.
ACCESSION   BZ463550
VERSION     BZ463550.1  GI:26749465
KEYWORDS    GSS.
SOURCE      Brassica oleracea
ORGANISM    Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 1044)
AUTHORS     Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
            Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE       Whole genome shotgun sequencing of Brassica oleracea and its
            application to gene discovery and annotation in Arabidopsis
JOURNAL     Genome Res. 15 (4), 487-495 (2005)
PUBMED      15805490
COMMENT     Other_GSSs: BONKC86TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES    Location/Qualifiers
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ORIGIN

Query Match        42.0%;     Score 616.6; DB 9;  Length 1044;
Best Local Similarity  77.3%;  Pred. No. 7.7e-179;
Matches  774;  Conservative   0;  Mismatches  224;  Indels   3;  Gaps        2;

Qy     455 ACAACTTATGATGGTACCGACAGAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGT 514
           ||||| |||||||| ||||||| |||||||||||||| |||| ||| | || ||| |||
Db    1007 AGAAGCAATGACGGTATCTGGGGAATAAGCATCGGCTAACTCTGTGCCAGCAGCCGCGGT 948

Qy     515 AATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGCAGGGCGCTT 574
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Db     947 AATACAGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCTGTAGGTGGCTT 888

Qy     575 TGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAATTGCGTTTGAAACTACAAAGC 634
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Db     887 TTTAAGTCCGCGTCAAATCCCAGGGCTCAACCCTGGGACAGGCGCGGTGGAAACTACCAAGC 828

Qy     635 TAGAGTGTAGCAGAGGGGGGGTGGAATTCCATGTGTAGCAGTGAAATGCGTAGAGATATGG 694
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Db     827 TTGAGTACGGTAGGGGCAGAGGGAATTTCCGGTGGCGGTGAAATGCGTAGAGATCGGA 768

Qy     695 AAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACTGACGCTCATGCACGAAAGCG 754
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Db     767 AAGAACACCAACGGCGAAGGCAGCCCCCTGGGTTGCTGCGGCCGAAACTGACACTGAGGAAGCT 708

Qy     755 TGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTT 814
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Db     707 AGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTACGCCGTAAACGATGGATACTAGGC 648

Qy     815 GTTGGGCCCTTACTAGGCTTG--GTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAG 872
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Qy     873 TACGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGATTAT 932
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Qy     933 GTGGATTAATTCGATGCAACGGCGAAAAACCTTACCTACCCTTGACATGTAGCGAATATTT 992
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Db     527 GTGGTTTAATTCGATGCAAGGGCGAAGAACCTTACCAGGGCTTGACATGCCGCGAATCCTC 468

Qy     993 TAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGTGCTGCATGGCTGTCGTCAGCT 1052
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Qy    1113 TCATTTAGTTGGGACTTTAATGACTGAGAATGCGGTTGACAAACCCGGGAAGTGGGGATGA 1172
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Db     227 AGGGTCGCGATCCCGCGAGGGTGCAGCTAACTCCTCAAAAACCGGTCCTCAGTTCGGATTGCA 168

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Qy    1412 AGAAGCAGATAGTCTAACCGTAGAGGGGCGTTTGCCACGGC 1452
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RESULT 9
BZ494182/c
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DEFINITION BONHR54TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONHR54,
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ACCESSION  BZ494182
VERSION    BZ494182.1  GI:27004681
KEYWORDS   GSS.
SOURCE     Brassica oleracea
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           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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REFERENCE  1  (bases 1 to 1051)
  AUTHORS  Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
           Utterback,T.R., Wortman,J.R. and Town,C.D.
  TITLE    Whole genome shotgun sequencing of Brassica oleracea and its
           application to gene discovery and annotation in Arabidopsis
  JOURNAL  Genome Res. 15 (4), 487-495 (2005)
   PUBMED  15805490
COMMENT    Other GSSs: BONHR54TF
           Contact: Chris Town
           TIGR
           9712 Medical Center Drive, Rockville, MD 20850, USA.
           Tel: 301-838-3523
           Fax: 301-838-0208
           Email: cdtown@tigr.org
           DNA is from a doubled haploid provided by Tom Osborn
           Seq primer: TR
           Class: sheared ends.
FEATURES             Location/Qualifiers
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                     total DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match        42.0%;     Score 616.6; DB 9;  Length 1051;
Best Local Similarity  77.3%;  Pred. No. 7.7e-179;
Matches  774;  Conservative   0;  Mismatches  224;  Indels   3;  Gaps        2;

Qy     455 ACAACTTATGATGGTACCGACAGAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGT 514
           ||||| |||||||| ||||||| |||||||||||||| |||| ||| | || ||| |||
Db    1007 AGAAGCAATGACGGTATCTGGGGAATAAGCATCGGCTAACTCTGTGCCAGCAGCCGCGGT 948

Qy     515 AATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGCAGGGCGCTT 574
           ||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||
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Db     827 TTGAGTACGGTAGGGGCAGAGGGAATTTCCGGTGGCGGTGAAATGCGTAGAGATCGGA 768

Qy     695 AAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACTGACGCTCATGCACGAAAGCG 754
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Db     767 AAGAACACCAACGGCGAAGGCAGCCCCCTGGGTTGCTGCGGCCGAAACTGACACTGAGGAAGCT 708
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Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES   Location/Qualifiers
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                     /organism="Nicotiana benthamiana"
                     /mol_type="mRNA"
                     /db_xref="taxon:4100"
                     /clone="NBMA117"
                     /tissue_type="abiotic and biotic stress-treated leaves,
                     callus tissue and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                     library, normalized, full-length"
                     /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                     supplier: RNA was isolated from Nicotiana benthamiana
                     tissues that include callus, roots from liquid culture
                     grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                     cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                     challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                     Xanthomonas campestris pv campestris 12 hr, 18hr;
                     Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                     campestris pv vesicatoria 18hr). RNA was isolated from
                     these tissues and pooled in approximately equal molar
                     amounts."

ORIGIN

Query Match   41.9%;   Score 614; DB 7; Length 889;
Best Local Similarity   82.3%;   Pred. No. 4.7e-178;
Matches 729; Conservative   0; Mismatches 155; Indels   2; Gaps   2;

Qy   1 TTGATCATGGCTCAGATTGAACGCTGGCGCCATGCTTACACATGCAAGTCAAGCGAACGGCAG   60
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Db   3 TTGATCATGGCTCAGATTGAACGCTGGCGCCTAACACATGCAAGTCAAGCGAGCGGCGCAG   62

Qy   61 CACGGGTGCTTGCACCTGGTGCGGAGTGCGGACGGTGAGTAATGCATCGGAACGTGTC 120
          |||||||||||||||||||||||||||||||||||| ||||||||||||||| || |||
Db   63 CACGGGTACTTGTACCTGGTGCGGAGCGCGGACGGTGAGTAATGCTAGGAATCTGCC 122

Qy   121 CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGAA 180
          ||||||||||||||| |||||||||||| |||| ||||||||| ||||||||||||||
Db   123 TGGTAGTGGGGGATAACGCTCGGAAACGGCGCTAATACCGCATACGTCTCCTACGGGAGAA 182

Qy   181 AGCAGGGGATCGAAAGACCTTGTCGTTTGGAGCGGCGCCCATGCGTCAGGTCGATCAGTAGTTGGT GGT 240
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   183 AGCAGGGGACCTTCGGGCCTTGCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGT GGT 242

Qy   241 GGGTAAAGCCTACCAAGGCAACGATCAGTAGTTCGTTCTGAGAGGACGAGCCAGCCACAC 300
          |||||||||| |||||||||||||||||||| ||||||||||||||||| |||||||||||
Db   243 GAGGTAATGCTCACCAAGGCTCACGATCCGATCCGTAACGTGTCTGAGAGGATGATCAGTCACAC 302

Qy   301 TGGGACTGAGACACGGCCCAGACTCCTACACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 360
          |||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||
Db   303 TGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATG 362

Qy   361 GGCGAAAGCCTGATCAGCAATGCCGCGGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTC 419
          |||||||||||||||||||| ||||||||||||||||||||||| ||||||||||||||
Db   363 GGCGAAAGCCTGATCAGCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCAC 422

Qy   420 TTTCAGTCGAGAGAAAGAAGGTTGACTAATATCACAACTTATGATGGTACCGACAGAA 479
          ||| || || ||||||||||||| |||| |||||||| || |||||||||||||
Db   423 TTTAAGTTGGGAGGAAGGGCAGTTACCTAATACGGATGATGTTTGACGTTACCGACAGAA 482

Qy   480 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 TAAGCACCGGCTAACTCGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATC 542

Qy   540 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTGTAAGTCAGATGGAATGAAATCCCGG 599
          |||||||||||||||||||| || ||||||| ||||| |||||||| |||||||||||||
Db   543 GGAATTACTGGGCGTAAAGCGCGTAGGCGGTTTGTTTGGTGGATGAAATCCCCGG 602

Qy   600 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAA 659

RESULT 10
CK280527
LOCUS   CK280527   889 bp   mRNA   linear   EST 02-AUG-2004
DEFINITION EST743249 Nicotiana benthamiana mixed tissue cDNA library,
            normalized, full-length Nicotiana benthamiana cDNA clone NBMA117 5'
            end, mRNA sequence.
ACCESSION   CK280527
VERSION   CK280527.1   GI:39850196
KEYWORDS   EST.
SOURCE   Nicotiana benthamiana
  ORGANISM Nicotiana benthamiana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1 (bases 1 to 889)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
            Staskawicz,B., Jin,H. and Baker,B.
  TITLE   Generation of EST sequences from Nicotiana benthamiana
  JOURNAL   Unpublished (2003)
COMMENT   Other ESTs: EST743250
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA

Qy   755 TGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTT 814
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   707 AGGGGAGCGAATGGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC 648

Qy   815 GTTGGGCCTTACTAGGCTTG--GTAACGTAGCTAGGTGAAGTTGACCGCCTGGGGAG 872
          |||||| ||| | ||||| ||||||| ||||||| ||||| ||||||||||||
Db   647 GCTGTCGTATCGACCCGTGCAGTCGTGTAGCTAACGCGTTAAGTATCCCGCCTGGGGAG 588

Qy   873 TACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTAT 932
          ||||| ||| | ||||| |||||||||||||||||||| |||||||||||||||||||||
Db   587 TACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCAT 528

Qy   933 GTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTGACATGTGTAGCGGAATATTT 992
          ||||| | ||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   527 GTGGTTTAATTCGATGCAAGCGAAGAGAACCTTACCAGGGCTTGACATGCCCGTCGTCAGCT 468

Qy   993 TAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCTGCATGGCTGTCGTCAGCT 1052
          || ||||||| ||||| ||||||||||||||||||||||||| | ||||||||||||||
Db   467 TTGAAAGAGAGGGGTGCCTTCGGGAACGGCACGCGACACAGGTGGTGCATGGCTGTCGTCAGCT 408

Qy   1053 CGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCATTAATTGCCA 1112
          |||||||||||||| ||||||||||||||||||||||||||||||||| || |||||||||
Db   407 CGTGCCGTAAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTGTTTAGTTGCCA 348

Qy   1113 TCATTTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGA 1172
          |||| | |||||||| ||||||||||||| |||||||||||||||||||||||||||||||
Db   347 CCGTTGAGTTTGGAACCCTGACACAGACTGCCGGTGATAAGCCGGAGGAAGGTGAGGATGA 288

Qy   1173 CGTCAAGTCCTCATGGCCCTTATGGTAGGGGCTTCACACGTAATACAAATGGCGCGTACAG 1232
          ||||||| ||||| ||| ||||||||||||| ||||| ||| |||||||||||||| ||
Db   287 CGTCAAGTCATCATGCCCCTTATGCCCGGGGCTGCACACGTGCTACAATGGCCGCGGACAA 228

Qy   1233 AGGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCCGGTCGTAGTCCGGATCGGA 1292
          ||||| ||||||||||||||||||||||| |||||| |||| ||||||||||||||||||
Db   227 AGGGTCGGATCCCGCGAGGGGGAGCTAATCCCGTCCTCAGTTCGGATTGCA 168

Qy   1293 GTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCGCGGATCAG-CATGTCGCG 1351
          ||||||||||||||||||||||||||||||||| ||||||||||||||| |||||||||
Db   167 GGCTGCAACTCGCCTGCATGAAGTCGGAATCGCTAGTAATCGCCGGTCAGCCATACGGCG 108

Qy   1352 GTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTTCACC 1411
          |||| ||||||||||||| || |||||||||||||||||| ||| ||||||| |||||||
Db   107 GTGAATTCGTTCCCGGGCCTTGTACACACCGCCCGTCACACTATGGGAGCTGGCCATGCC 48

Qy   1412 AGAAGCAGATAGTCTAACGTAAGAGGGCGTTTGCCACGGC 1452
          |||| | | | |||||| |||| ||||| |||
Db   47 AAAAGTCGTTACCTTAACCGGAAGGAGGGGGGGGGCCGAAGGC 7

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Qy   335 GCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCCGTGAGTG 394
             |||||||||||||||||||   |||||||||||||||||||||||||||||||||||||
Db   895 GCAGCAGTGGGGAATTTTCCG--CAATGGGCGAAAGCCTGATCCAGCAATGCCGCCGTGAGG 837

Qy   395 AAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGCAGAAGAAGAAAGGTTGTGACTAATAAT 453
             |||||| ||| ||||  |  |  |||||||  |||| ||||
Db   836 TAGAAGGCCTACGGGTCCTGAACTTCTTTCCCAGAGAAG---------------- 797

Qy   454 CACCAACTTATGATGGTACCGACAGAGAAGAGCACCGGCTAACTACGTGCCAGCAGCCGCGG 513
               | |  |  ||  | ||| |  |  ||||  | |||||||||||  |||| ||||||||||
Db   796 ---AAGCAATGACACGGTATCTGGGGGAATAAGCATCGGCTAACTCGTGTCGTCCAGCAGCCGCGG 740

Qy   514 TAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCT 573
         ||||||  | ||  |||||||||| ||||||  | ||||| |||| | | | | | |||||
Db   739 TAATACAGAGGATGCAAGCGTTATCCGGAATGATTGGGCGGTAAAGCGTCGTGTAGGTGGCT 680

Qy   574 TGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAATTGCGTTGAAACTACAAAG 633
         | |||||||  | | ||||||| ||||| ||||  ||   ||||| ||||||| |||||
Db   679 TTTTAAGTCCGCGTCAAATCCCAGGGCTCAAACCCTGACAGGCGGTGAAACTTACCAAG 620

Qy   634 CTAGAGTGTAGCAGAGGGGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATATG 693
         || |||| | | ||||||   ||||| |  |||| ||||||||||||||||||||| ||
Db   619 CTTGAGTACGGTAGGGGCAGAGGGGAATTTCCGGTGGCAGCGGTGAAATGCGTAGAGATCGG 560

Qy   694 GAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACTGACGCTCATGCACGAAAGC 753
         |||||||| |  |||||| ||| ||| | ||||   ||||||||||| || ||||||||||
Db   559 AAAGAACACCAACCGCGAAAGCACTCTGCTGGGCCGACACTGACACTGAGAGACGAAAGC 500

Qy   754 GTGGGGAGCAAACGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGTCAACTAGT 813
          |||||||||| | |||||||||||||  |||||| | |||||||||||||| ||||  |
Db   499 TAGGGGAGCGAATGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGATGACTACTAGG 440

Qy   814 TGTTCGGGCCTTACTAGGCTTG--GTAACGTAGCTAACGGTGAAGTTGACCGCCTGGGGA 871
          |  | |||| ||| |  | || | | |    |||| ||||||| | |||| | ||||||
Db   439 CGCTGTGCCGTATCGACCCGTGCAGTGCGTCGCCTTAAGTATCCCGCCTGGGGGA 380

Qy   872 GTACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGACCCCACAAGCGGTGGATTA 931
         ||||| |||||| | |||||||||||||||||||||||| |||| ||||||||||| ||
Db   379 GTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGCCCCGCACAAGCGGTGGAGCA 320

Qy   932 TGTGATTAATTCGATGCAACGCGAAAAACCTTACCTCCCTTGACATGCATGAATATT 991
         ||||| | ||||||||||| |||||| |||||||||  | ||||||||| ||||  |
Db   319 TGTGGTTTAATTCGATGCAAACGCGAAGAACCTTACCAGGGCTTGACATGCCGAATCCT 260

Qy   992 TTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCTGCATGGCTGTCGTCAGC 1051
          | |||| |   | |||||||||||||||| |  | |||||| |||||||||||||||||
Db   259 CTTGAAAGAGGGGGTGCCTTCGGGAACGCGGATGAACGCAGTGGTGCATGGCTGTCGTCAGC 200

Qy  1052 TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACCCTTGTCATTAATTGCC 1111
         ||||| ||| |  ||||||||||||||||| |   ||| |  | | |||||
Db   199 TCGTGCCGTAGGTGTTGGGTTAAGTCCCGTGTTTTTAGTTGCC 140

Qy  1112 ATCATTTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACCGGAAGGTGGGGATG 1171
          || ||| | |||| | | ||| |  | ||||||  || |  |||| || || |||
Db   139 ACCGTTGAGTTTGGAACCCTGAACCCTGATAAGCCGGGATAAGGCGGAAGGTGAGGATG 80

Qy  1172 ACGTCAAGTCATCATGGCCCTTATGGGTAGGGCTTCACACGTAATACAATGGCCGGTACA 1231
         | |||||||||||||| |||||||| | |||||  ||||||| |||||||||||| |||
Db    79 AGGTCAAGTCATCATGCCCCTTATGCCCTGGGCGACACACGTGCTACAATGGCCGGACA 20

Qy  1232 GAGGGTTGCCAACCCGCGA 1250
         |||||||| || ||||||
Db    19 AAGGGTTCGCGATCCCGCGA 1
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Db   603 GCTCAACCTGGGAACTGCATCCAAAACTGGCAAGCTAGAGTATGTGGTAGAGGGGGTGTGA 662
             |||| || |  || |  |  |||   ||| | | | | | | |
Qy   660 TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC 719
         ||||| |||||||| |||||||||||||  || |||||||||| |  ||||||||| |||
Db   663 TTTCCTGTGTGTAGCGGTGAAATGCGTAGATATAGGAAGAACACCAGTGGCGAAGGCGACC 722

Qy   720 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 779
          ||||||  |||  |||||||| || | |||||||||||||||||||||||||||||||||
Db   723 ACCTGGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC 782

Qy   780 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGG--CCTTACTAGGCTTGGTAA 838
         |||||||||||||||||||||||||||||||| ||||| ||  |||| |  | |||
Db   783 CTGGTAGTCCACGCCCTAAACGATGTCAACTAACTAGCCGTTGGGAGCCTTGGAGCTCTTAGTGG 842

Qy   839 CGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAG 884
         || |||||||| | |||||||||||||||||||||||||||||  |
Db   843 CGCAGCTAACGCATTAAGTTGACCGCCTGGGGAGTACGGTCGCGCAAG 888
```

RESULT 11
BZ426201/c
LOCUS   BZ426201   1016 bp   DNA   linear   GSS 13-DEC-2002
DEFINITION BONDZ28TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONDZ28,
            genomic survey sequence.
ACCESSION   BZ426201
VERSION   BZ426201.1 GI:26667713
KEYWORDS   GSS.
SOURCE   Brassica oleracea
  ORGANISM Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 1016)
  AUTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
            Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
  TITLE   Whole genome shotgun sequencing of Brassica oleracea and its
            application to gene discovery and annotation in Arabidopsis
  JOURNAL   Genome Res. 15 (4), 487-495 (2005)
  PUBMED   15805490
COMMENT   Other GSSs: BONDZ28TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES   Location/Qualifiers
     source   1..1016
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BONDZ28"
                     /clone_lib="BO_1.6_2_KB_tot"
                     /note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared
                     total DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

Query Match   41.8%; Score 613.8; DB 9; Length 1016;
  Best Local Similarity   77.5%; Pred. No. 5.6e-178;
  Matches 805; Conservative   0; Mismatches 207; Indels 27; Gaps   4;

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Qy   215 GGCCGATGCCTGATTAGCTAGTTGGTGGGTAAAGGCCTACCAAGGCAACGATCAGTAGT 274
         ||| | || ||||||||||||||||||||| | ||||   |  |||||||||||||||
Db  1015 GGCTCGCGTCTGATTAGCTAGTTGGTGGGTGAGGCAATAGTCTTACCAAGGCGATGATCAGTAGC 956

Qy   275 TGGTCTGAGAGGACGACCACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG 334
         ||||| ||||||| || |||||||||||||||||||||||||||||||||||||||||||||
Db   955 TGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG 896
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RESULT 12
BH705272
LOCUS   BH705272   1079 bp   DNA   linear   GSS 20-FEB-2002
DEFINITION BOMKA47TF BO_2_3_KB Brassica oleracea genomic clone BOMKA47,
            genomic survey sequence.
ACCESSION   BH705272
VERSION   BH705272.1 GI:18787746

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Db    508 ATCGGAAAGAACACCAACCGGCAAAGCACTCTGTGGGCCGACACTGACACTGAGAGACG 567

Qy    749 AAAGCGTTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCAGTCCAGGGCCCTAAACGATGATGTCAA 808
          |||||||  ||||||||||  ||||||||||||||||||||||  |||||  |||||||||||||||||||
Db    568 AAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATA 627

Qy    809 CTAGTTGTTGGGCCTTACTAGGCTTG--GTAACGTAGCTAACGGCTAACGGTGACCGCCT 866
          ||||  |||||||||||||||||||||  |||||||  ||||  ||||||||||||||||||
Db    628 CTAGGGCGTGTGGTATCGACCCGTGCAGTGGTGCTGTAGCTAGTCAACGGTTAAGTATCCCGCCT 687

Qy    867 GGGGAGTACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTG 926
          |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db    688 GGGGAGTACGGTCGCAAGATTAAAACTCAAGGAATTGACGGGGGCCCCACAAGCGGTG 747

Qy    927 GATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGGTAGCGA 986
          ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 GAGCATGTGGTTTAATTCGATGCAAGCGAAGAACCTTACCACAGCGGCTTGCATGGCTGTCG 807

Qy    987 ATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGTGCTGCGTCGCATGGCTGTCG 1046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 ATCCTCTTGAAAGAGAGAGGGTGCGTTCGGGAACCGGACACAGTGGTGCATGGCTGTCG 867

Qy   1047 TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCATTAA 1106
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    868 TCAGCTCGTGCCGTAAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTGTTTAG 927

Qy   1107 TTGCCATCATTTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAAACCGGAGGAAGGTGG 1166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    928 TTGCCACCGTTGAGTTTGGAACCCCTGACACAGTGCCGGTGATAGCCGGAGGAAGGTGA 987

Qy   1167 GGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACAGTAATACAATGGCGC 1226
          |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db    988 GGATGACGTCAAGTCATCATGCCCCTTATGCCCTGGGCGACACACGTGCTATCATGGCCG 1047

Qy   1227 GTACAGAGGGTTGCCAACCCGCGAGGGGGAGC 1258
          ||||||||||||||||||||||||||||||||
Db   1048 GGACAAAGGGTCGCGATCCCGCGGAGGGGTGAGC 1079
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RESULT 13
BH656222/c

LOCUS   BH656222   1031 bp   DNA   linear   GSS 19-FEB-2002
DEFINITION BOMZ86TF BO_2_3_KB Brassica oleracea genomic clone BOMZ86,
            genomic survey sequence.
ACCESSION   BH656222
VERSION   BH656222.1 GI:18714532
KEYWORDS   GSS.
SOURCE   Brassica oleracea
ORGANISM   Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 1031)
AUTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
            Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE   Whole genome shotgun sequencing of Brassica oleracea and its
            application to gene discovery and annotation in Arabidopsis
JOURNAL   Genome Res. 15 (4), 487-495 (2005)
PUBMED   15805490
COMMENT   Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES   Location/Qualifiers
     source   1..1031
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"

ORIGIN

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Query Match      41.8%;  Score 613.2;  DB 9;  Length 1079;
Best Local Similarity   76.3%;  Pred. No. 8.7e-178;
Matches  803;  Conservative   0;  Mismatches 223;  Indels  26;  Gaps   3;

Qy    210 GGAGCGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCTACCAAGGCAACGATCA 269
          |||||   ||  |  |||||||||||||||||||||||||||  | ||||||||||||
Db     51 GGAGGGGCTCGCGTCTGATTAGCTAGTTGGTGGGGCAATAGCTTACCAAGGCGATGATCA 110

Qy    270 GTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTAC 329
          ||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db    111 GTAGCTGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTAC 170

Qy    330 GGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGT 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 GGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATGCCGCGT 230

Qy    390 GAGTGAAGAAG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGAAAAGGTTGTGACTA 448
          ||||||||||| |||||||||||||||||||   |||  |||||||||||
Db    231 GCGAGGTAGAAGGCCTACGGGTCCTGAACTTCTTTTCCCAGAGAAG------------- 275

Qy    449 ATAATCACACTTATGATGGTACCGACAGAGAAGACACCGGCTAACTACGTGCCAGCAGC 508
          |||||||||| | ||| || |||||||||||||||||||| |||||||| |||||||||
Db    276 -------AAGCAATGACGGTATCTGGGGAATAAGCATCGGCTAACTCTGTGCCAGCAGC 327

Qy    509 CGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGCAGG 568
          ||||||||||||||||||||||||||| ||||||||||||||||||||||| ||| ||||
Db    328 CGCGGTAATACGTAGGGTGCAAGCGTTATCCGGAATTGGGCGTAAAGCGTCTGTGTAGG 387

Qy    569 CGGCTTTGTAAGTCACGATGTGAAATCCCCGGGCTTAACCTGGGAATTGCGTTGAAACTA 628
          |||||||| ||| ||  ||||||||||||||||||||||||  ||||| ||||| |||||
Db    388 TGGCTTTTTAAGTCCGCCGTCAAATCCCAGGCGCTCAACCTGGACAGGCGGTGGAAACTA 447

Qy    629 CAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAGTGAAATGCGTAGAG 688
          |||||||||  ||   ||||||||||||||||||||||||||||| |||||||||||||
Db    448 CCAAGCTTGAGTGTCGGTAGGGGCAGAGGGAATTTCCGGTGGCGGGAAATGCGTAGAG 507

Qy    689 ATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACTGACGCTCATGCACG 748
          || ||||||  ||  ||| ||||||||||  |||| |  |||  ||| |||||  ||||||
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Fri Apr 7 06:40:06 2006

Db   154 AATGGCCGGACAAAGGGTCGCGATCCCCGGAGGGTGAGCTAACTCCAAAAACCCGTCCT 95

Qy   1279 TAGTTCCGGATCGGAGTCTCGAACTCGACTCCGTGAAGTCCGGAATCGCTAGTAATCGCGGA 1338
Db   94 CAGTTCGGATTCGAGCGTGCAACTCGCCTGCATGGAAGTCGTTCCCGGGCCT 35

Qy   1339 TCAGCATGTCGCGGTGAAATACGTTCCGGGTCT 1371
Db   34 TCAGCCATACGGCGGAATTCGTTCCCGGGCCT 2

RESULT 14
BZ450751
LOCUS   BZ450751   1077 bp   DNA   linear   GSS 13-DEC-2002
DEFINITION BONBQ63TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONBQ63,
            genomic survey sequence.
ACCESSION   BZ450751
VERSION   BZ450751.1 GI:26721334
KEYWORDS   GSS.
SOURCE   Brassica oleracea
  ORGANISM Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 1077)
  AUTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
            Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
  TITLE   Whole genome shotgun sequencing of Brassica oleracea and its
            application to gene discovery and annotation in Arabidopsis
  JOURNAL   Genome Res. 15 (4), 487-495 (2005)
   PUBMED   15805490
COMMENT   Other GSSs: BONBQ63TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES   Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone_lib="BONBQ63"
                     /clone_lib="BO_1.6_2_KB_tot"
                     /note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
                     total DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

Query Match   41.7%; Score 611.6; DB 9; Length 1077;
Best Local Similarity 76.9%; Pred. No. 2.7e-177;
Matches 772; Conservative 0; Mismatches 229; Indels 3; Gaps 2;

Qy   455 ACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCCGGT 514
          ||| ||| || || |||| || |||||| ||||| ||| |||| || |||||| ||| ||
Db   61 AGAAGCAATGACGTATCTGGGGAATAAGCATCGGCTAGTAACCTCTGTGCCAGCAGCCGCGT 120

Qy   515 AATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTT 574
          |||| ||| | ||| |||||| ||| || ||| || |||||| || ||||||||
Db   121 AATACAGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCTGTAGGTGGCTT 180

Qy   575 TGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAATTGCGTTTGAAACTACAAAGC 634
          |||| |||| || ||||||||||||| ||||| ||| |||| || || ||| || ||
Db   181 TTTAAGTCCGGCCGTCAAATCCCCAGGCTCAACCTGGGAATTGCGGTCGGTGAAACTACCAAGC 240

Qy   635 TAGAGTGTAGCAGAGGGGGGTTGGAATTCCATGTGTAGCAGTGAAATGCGTAGATATGG 694
          ||||| || || |||||| | || |||||| || |||| |||||||||||||| |||
Db   241 TTGAGTACGGTAGGGGCAGAGGGAATTTCCGGTGGAGCGGTGAAATGCGTAGAGATCCGGA 300

ORIGIN

Query Match   41.8%; Score 612.6; DB 9; Length 1031;
Best Local Similarity 76.3%; Pred. No. 1.3e-177;
Matches 803; Conservative 0; Mismatches 224; Indels 26; Gaps 3;

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/clone="BOMJ286"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

Qy   322 ACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCAA 381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 ACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGGAAAGCCTGACGGAGCAA 972

Qy   382 TGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGGAGAAGAAAAGT 440
          |||||||||||||||||||| |||||||||||||| || || |||||| ||||||||
Db   971 TGCCGCGTGAGTGAAGAAGGTAGAAGGCTCACGGCGTCCGAACTTCTTTCCCAGAGAAG------- 919

Qy   441 TGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAACTACGTG 500
             ||| || ||||| ||||||||| || || |||||| || ||| |||| | ||
Db   918 --------AAGCAATGACGTATCTGGGGAATAAGCATCGGCTAGTAACCTCTGTG 875

Qy   501 CCAGCAGCCGCCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGG 560
          ||||||||||| ||||||||| ||||||||||||||| |||||||| |||||||||| |
Db   874 CCAGCAGCCGCGGTAATACAGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCG 815

Qy   561 TGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAATTGCGTT 620
          || ||||||||||| |||| |||| || ||||||||| ||||||| ||||||||||||
Db   814 TCTGTAGGTGGCTTTTTAAGTCCGGCCGTCAAATCCCCAGGGCTCAACCTGGGACAGCGGT 755

Qy   621 TGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTTGGAATTCCATGTGTAGCAGTGAAAT 680
          ||||||||| || || |||| || ||||||| | || |||||||| ||||| |||||||
Db   754 GGAAACTACCAAGCTTGAGTACGGTAGGGGCAGAGGGAATTTCCGGTGGAGCGGTGAAAT 695

Qy   681 GCGTAGAGATATGGAAGAACAATCGATGGCGAAGGCAGCCCCCTGGGTTAACACTGACGCT 740
          |||||||||| | || |||| || ||||||||||||||||| ||| || || |||
Db   694 GCGTAGAGATCGGAAGAACACCAACGGCGAAAGCACTCTGCTGGGCCGAAAGCACTGACACT 635

Qy   741 CATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC 800
          |||||||||||||| ||||||||| |||||||||| ||||||||||||| |||||||||
Db   634 GAGAGACGAAAGCTAGGGGAGCGAATGGGATTAGATATCCCAGTAGTCCTAGCCGTAAAC 575

Qy   801 GATGTCAACTAGTTGTTGGGCCTTACTAGGCTTG--GTAACGTAGCTAACGCGTGAAGTT 858
          ||||| ||| || |||||| |||| |||||| ||| || |||| |||||||| ||
Db   574 GATGGATACTAGGCGCGTGTCTATCGACCCGTGTAGTGCTGTGTAGCTAACGCGTTAAGTA 515

Qy   859 GACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGCAC 918
          || ||||||||||||||| | | ||| ||||| |||||||||||| |||||| || |||
Db   514 TCCCGCCTGGGGAGTACGGTCGCAAGATTCAAGAGAATGAAACTCAAAGGAATTGACGGGGGCCCGCAC 455

Qy   919 AAGCGGTGGAGTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTGGTCTTGACA 978
          ||||||||||||| | ||||||||||||| |||||||||||| ||||| ||| |||||
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Qy   979 TGTAGCGAATATTTTAGAGATAAAAATAGTGCCTTCGGGAACGCTAACACACAGGTGCTGCAT 1038
          || || ||| ||| || ||| |||| |||| |||||||| || || |||||| || ||||
Db   394 TGCCGCGGAATCCTCTTCTGAAAGAGAGGGTGCCTTCGGGAACGCGAACACAGGTGGTGCAT 335

Qy   1039 GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTT 1098
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Db   334 GGCTGTCGTCAGCTCGTGTCGTGAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTC 275

Qy   1099 GTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACCGGAG 1158
          || ||||| || |||| || | ||||| | |||| || |||| || ||||| ||| ||
Db   274 GTGTTTAGTTGCCACCGTTGAGTTGGGCAACTTCCCGGTTGATAGCGGGAG 215

Qy   1159 GAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTAATAC 1218
          ||||| || ||||||||||||| || |||||||| | | ||||| ||||||||||||
Db   214 GAAGGTGAGGATGACGTCAAGTCATCATGCCCCTTATGCCTGGGCGACACAGTGCTAC 155

Qy   1219 AATGGCCGGTACAGAGGGCTACAACCCCGGGAGGGGGGGAGCTAATCTCAGAAAGCGCCTCG 1278
          ||||| || ||||||||| ||||||||||||| |||| |||||||||||||||||||||||
Db   1278

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES   Location/Qualifiers
source   1..884
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                /mol_type="mRNA"
                /db_xref="taxon:4100"
                /clone="NBMA117"
                /tissue_type="abiotic and biotic stress-treated leaves,
                callus tissue and root tissue"
                /lab_host="DH10B-TonA"
                /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                library, normalized, full-length"
                /note=Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                supplier: RNA was isolated from Nicotiana benthamiana
                tissues that include callus, roots from liquid culture
                grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                Xanthomonas campestris pv campestris 12 hr, 18hr;
                Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                campestris pv vesicatoria 18hr). RNA was isolated from
                these tissues and pooled in approximately equal molar
                amounts."

ORIGIN

Query Match   41.6%; Score 610; DB 7; Length 884;
Best Local Similarity 82.2%; Pred. No. 8.1e-177;
Matches 725; Conservative 0; Mismatches 155; Indels 2; Gaps 2;

Qy   1 TTGATCATGGCTCAGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCAAGTGCAACGGCAG 60
           ||||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||
Db   3 TTCATCATGGCTCAGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCAAGTGCAACGGCAG 62

Qy   61 CACGGGTCTTGCACCTGGTGCGAGTGCGCGGCGGACGGGTGAGTAATGCATCGGAACGTGTC 120
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Db   63 CACGGGTACTTGTACCTGGTGCGAGTGCGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCC 122

Qy   121 CAGAAGTGGGGATAACGCATCGAAAGATGTGTAATACCGCATATTCTCTACGGAGGAA 180
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Db   123 TGTAGTGGGGATAACGCTCGGGAAACGACGCTAATACCGCATACGTCCTACCGGGAGAA 182

Qy   181 AGCAGGGGATCGAAAGACCTTGGTGCTTTGGAGCGGCGGCCGATGCCTGATTAGCTAGTTGGT 240
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   183 AGCAGGGGACCTTCGGGCCTTGCGCTATCAGATGAGCCTAGGTCGGATTCGGAATTGGT 242

Qy   241 GGGGTAAGGCCTACCAAGGCAACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACAC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   301 TGGGACTGAGACACGGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 360
           ||||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||||
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Qy   361 GGCGAAAGCCTGATCCAGCCATGCCGCGTGAGTGAAGAAGG--CTTCGGGTTGTAAAGCTC 419
           ||||||||||||||||||||||||||||||| || ||||||||||||||||||||||
Db   363 GGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGGTTGTAAAGCAC 422

Qy   420 TTTCAGTCGAGAGAAAAGGTTGTGACTAATATCACAACTTATGATGGTACCGACAGAA 479
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423 TTTAAGTTGGGAGGAAGGGCAGTTACCTAATACGATTGTTTGACGTTACCGACAGAA 482

Qy   480 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 TAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATC 542

Qy   540 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGTTGTAAGTCAGATGTGAAATCCCCGG 599
           ||||||||||||||||| || ||| |||||||||||||||||||||||||||||||||

Qy   695 AAGAAACATCGATGGCGAGGCAGCCCCCTGGGTAACACTGACGCTCATGCACGAAAGCG 754
           |||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   301 AAGAAACAACCAACGGGCGAAAGCACTCTGCTGGGCCGACACTGACACTGAGAGACGAAAGCT 360

Qy   755 TGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTT 814
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Db   361 AGGGGAGCGAGCGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC 420

Qy   815 GTTGGGCCTTACTAGGCTTG--GTAACGTAGCTAACGGTGAAGTTGACCGCCTGGGGAG 872
           | ||||||||||||||||||| |||| |||| |||||||||||||||||||||||||||
Db   421 GCTGTGCGTATCGACCCGTGCAGTCGCGTGTAGCTAACGGTGAAGTATCCCGCCTGGGGAG 480

Qy   873 TACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTAT 932
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   481 TACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCAT 540

Qy   933 GTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGTAGCGGAATATTT 992
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Db   541 GTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAGGGCTTGACATGCCGGGAATCCTC 600

Qy   993 TAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGTGCTGCACACAGGTGCTGCGTCGTCAGCT 1052
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Qy   1053 CGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCATTAATTGCCA 1112
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Db   661 CGTGCCGTAAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTCGTGTTTAGTTGCCA 720

Qy   1113 TCATTTAGTTGGGCACTTAATGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGA 1172
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Db   721 CCGGTTTGGTTTGGAACCCTGCGACACAGTGCCGGTGATAAGCCGGAGGAAGGTGAGGATGA 780

Qy   1173 CGTCAAGTCCTCATGGGCCCTTATGGGTAGGGCTTCACACGTAATATCAATGGCGGTACAG 1232
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Db   781 CGTCAAGTCATCATGGCCCTTATGCCCTGGGCGACACACGTGCTACAAGTGCCGGGACAA 840

Qy   1233 AGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGCGTCGTAGTCCGGATCGGA 1292
           |||||||||||||||||||||||||||| ||| |||||||||| ||| |||||||
Db   841 AGGGTTGCGCGATCCCGCGAGGGCGAAGGTGAGCTAACTAACCGGTCCGTCCAGTTCGGATTGCA 900

Qy   1293 GTCTGCAACTGACTCCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAG-CATGTCGCG 1351
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Db   901 GGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGCCGGTCAGCCATACGGCG 960

Qy   1352 GTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTTCACC 1411
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Qy   1412 AGAAGCAGATAGTCTAACCGTAAGGAGGCGTTTGCCACGGCGAG 1455
           |||||||||| |||||| ||||| ||| | ||
Db   1021 CGAAAGTGCTACCTTAACCCGCAGGAGGGGGGTGCCGAAGGCAG 1064

RESULT 15
CK280528

LOCUS   CK280528   884 bp   mRNA   linear   EST 02-AUG-2004
DEFINITION EST743250 Nicotiana benthamiana mixed tissue cDNA library,
            normalized, full-length Nicotiana benthamiana cDNA clone NBMA117 5'
            end, mRNA sequence.
ACCESSION   CK280528
VERSION   CK280528.1   GI:39850200
KEYWORDS   EST.
SOURCE   Nicotiana benthamiana
  ORGANISM Nicotiana benthamiana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1 (bases 1 to 884)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
            Staskawicz,B., Jin,H. and Baker,B.
  TITLE   Generation of EST sequences from Nicotiana benthamiana
  JOURNAL   Unpublished (2003)
COMMENT   Other_ESTs: EST743249

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Db     543 GGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTGTTAAGTTGGATGTGAAATCCCCGG 602

Qy     600 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA 659
            ||  || ||||||||| ||| |   ||||  |||||||||| ||  | ||||| ||||||
Db     603 GCTCAACCTGGGAACTGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAA 662

Qy     660 TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC 719
            |||| | |||||||||| || || || | |   |  |||   | |||||| |||||| ||
Db     663 TTTCCTGTGTAGCGGTGAAATGCGTAGATATTAGGAAGGACACCAGTGGCGAAGGCGACC 722

Qy     720 CCCTGGGTTAACACTGACGGTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 779
            |||||  |     ||||||||||    |  |||||||||||||||||||||||||||||
Db     723 ACCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC 782

Qy     780 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGG-CCTTACTAGGCTTGGTAA 838
            ||||||||||||||| ||||||||||||||  |  || |     ||| ||||| || ||
Db     783 CTGGTAGTCCACGCCGTAAACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGG 842

Qy     839 CGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCG 880
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Db     843 CGCAGCTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCG 884


Search completed: April 6, 2006, 21:18:42
Job time : 6264 secs
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                    Copyright   GenCore version 5.1.7
                    (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:   April  6, 2006, 19:23:40 ; Search time 295 Seconds
                                      (without alignments)
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Title:           US-10-659-983A-18
Perfect score:   1467
Sequence:        1 ttgatcatggctcagatga........acggcgagattcatgagactgg 1467
Scoring table:   IDENTITY_NUC
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Searched:        1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters:    2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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    5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1115	76.0	1536	2	US-08-642-229A-1	Sequence 1, Appli
2	1104	75.3	1536	2	US-08-114-695A-7	Sequence 7, Appli
3	1092.2	74.5	1474	2	US-08-114-695A-8	Sequence 8, Appli
4	1090.4	74.3	1544	3	US-09-726-774-5	Sequence 5, Appli
c 5	1084.8	73.9	1453	3	US-09-735-567-4	Sequence 4, Appli
6	1081.6	73.7	1455	2	US-08-642-229A-3	Sequence 3, Appli
7	1078.2	73.5	1451	3	US-09-342-579-1	Sequence 1, Appli
8	1078.2	73.5	1451	3	US-09-617-854A-1	Sequence 2, Appli
9	1066.8	72.7	1452	2	US-08-642-229A-2	Sequence 2, Appli
10	1054.6	71.9	1495	3	US-09-063-898-1	Sequence 1, Appli
11	1054.6	71.9	1495	3	US-09-985-846-1	Sequence 2, Appli
c 12	1049.2	71.5	1467	3	US-09-735-567-2	Sequence 6, Appli
c 13	1048.4	71.5	1539	3	US-09-735-567-6	Sequence 7, Appli
14	1047.8	71.4	1454	3	US-09-735-567-7	Sequence 1, Appli
15	1037.6	70.7	1540	3	US-09-228-184-1	Sequence 1, Appli
16	1037.6	70.7	1540	3	US-09-967-376-1	Sequence 3, Appli
17	1025.4	69.9	1450	3	US-09-735-567-3	Sequence 53, Appl
18	1012.6	69.0	1484	2	US-08-613-470-53	Sequence 4, Appli
19	1012.4	69.0	1481	3	US-09-737-297-4	Sequence 5, Appli
20	1008.2	68.7	1501	3	US-09-793-920A-1	Sequence 1, Appli
21	1008.2	68.7	1501	3	US-09-821-016-5	Sequence 1, Appli
22	1008.2	68.7	1501	3	US-09-745-476-1	Sequence 1, Appli
23	1008.2	68.7	1501	3	US-09-748-205-1	Sequence 1, Appli
24	1008.2	68.7	1501	3	US-09-951-720-1	Sequence 1, Appli
25	1008.2	68.7	1501	3	US-10-411-319-1	Sequence 1, Appli
26	1008.2	68.7	1501	3	US-10-105-305-1	Sequence 1, Appli
27	1008.2	68.7	1501	3	US-10-266-787-5	Sequence 5, Appli
28	1008.2	68.7	1501	3	US-09-791-610-1	Sequence 1, Appli
29	1008.2	68.7	1501	3	US-10-252-518-5	Sequence 5, Appli
30	1001.6	68.3	1518	2	US-08-114-695A-6	Sequence 6, Appli
31	997.8	68.0	1449	3	US-09-602-417-1	Sequence 1, Appli
32	992.2	67.6	1486	3	US-09-737-297-1	Sequence 41, Appl
c 33	989.4	67.4	269223	3	US-09-596-002-41	Sequence 12, Appl
34	986.2	67.2	1424	3	US-10-007-527A-12	Sequence 3, Appli
35	982.8	67.0	1467	3	US-09-726-774-3	Sequence 2, Appli
36	981.2	66.9	1541	3	US-09-726-774-2	Sequence 1, Appli
c 37	979.2	66.7	1830121	3	US-09-557-884-1	Sequence 1, Appli
38	979.2	66.7	1830121	3	US-09-557-884-1	Sequence 1, Appli
c 39	979.2	66.7	1830121	3	US-09-643-990A-1	Sequence 1, Appli
40	979.2	66.7	1830121	3	US-09-643-990A-1	Sequence 1, Appli
c 41	979.2	66.7	1830121	3	US-10-158-865-1	Sequence 1, Appli
42	979.2	66.7	1830121	3	US-10-158-865-1	Sequence 1, Appli
43	978.2	66.7	1542	2	US-08-757-653-158	Sequence 158, App
44	978.2	66.7	1542	3	US-09-465-355-2	Sequence 2, Appli
45	978.2	66.7	1542	3	US-08-520-946-158	Sequence 158, App

ALIGNMENTS

```
RESULT 1
US-08-642-229A-1
; Sequence 1, Application US/0864229A
; Patent No. 5874291
GENERAL INFORMATION:
  APPLICANT:  Herwig, Russell P.
  APPLICANT:  Bielefeldt, Angela R.
  APPLICANT:  Stensel, H. David
  APPLICANT:  Strand, Stuart E.
  TITLE OF INVENTION:  Degradation of Environmental Toxins by a
  TITLE OF INVENTION:  Filamentous Bacterium
  NUMBER OF SEQUENCES:  10
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Christensen O'Connor Johnson and Kindness PLLC
    STREET:  1420 Fifth Avenue, Suite 2800
    CITY:  Seattle
    STATE:  Washington
    COUNTRY:  USA
    ZIP:  WA 98101-2347
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/642,229A
    FILING DATE:
    CLASSIFICATION:  435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/246,865
    FILING DATE:  20-MAY-1994
  ATTORNEY/AGENT INFORMATION:
    NAME:  Sheiness, Diana K.
    REGISTRATION NUMBER:  35,356
    REFERENCE/DOCKET NUMBER:  UOFW19233
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (206) 682 8100
    TELEFAX:  (206) 224 0779
    TELEX:  4938023
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  1536 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  nucleic acid
    DESCRIPTION:  "16S ribosomal DNA"
```

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;  HYPOTHETICAL: NO
;  ANTI-SENSE: NO
;  ORIGINAL SOURCE:
;    ORGANISM: Comamonas testosteroni ATCC No. 5874291 11996
US-08-642-229A-1

Query Match     76.0%;  Score 1115;  DB 2;  Length 1536;
Best Local Similarity  87.2%;  Pred. No. 0;
Matches 1282;  Conservative  0;  Mismatches  180;  Indels  9;  Gaps  5;

Qy        1  TTGATCATGGTCAGATTGAACGCTGGCGCGATGCTTTACACATGCAAGTCGAACGGCAG    60
             ||||| |||||||||||||||||||||||||||||  |||||||||||||||||||||||
Db       14  TTGATCCTGGCTCAGATTGAACGCTGGCGGCGTGCTTACACATGCAAGTCGAACGGTAA    73

Qy       61  CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC   120
             ||| |       ||||||| |||||||||||||||||||||||||||||||||||||||
Db       74  CA---GGTCTTCGGATGCTGACGAGTGGCGAACGGGTGAGTAATACATCGGAACGTGCC   129

Qy      121  CAGAAGTGGGGGATAACGCATCGAAAGATGCTAATACCGCCATATTCTCTACGGAGGAA   180
             ||||||||||||||   ||  ||||||||||||||||||||||||
Db      130  TAGTAGTGGGGGATAACTACTCGAAAGAGTAGCTAATACCGCATGAGATCTACGGATGAA   189

Qy      181  AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT   240
             ||||||||||||||||||||| |||| ||   ||| |    |  ||||||||||||||||
Db      190  AGCAGGGGGATCGGCTTCGGGCCGTTGTGCTGTACTAGCGGCTGTGATTAGCTAGTTGGT   249

Qy      241  GGGGTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC   300
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      250  GGGGTAAAGGCCTACCAAGGCGTTACCAAGCCTGCGATCTGTGAGAGGACGACCAGCCACAC   309

Qy      301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG   360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      310  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG   369

Qy      361  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG--CTTCGGGTTGTAAAGCTC   419
             |||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db      370  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCCTCGGGTTGTAAACTGC   429

Qy      420  TTTCAGTGTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA   479
             |||| |  |   || |  |  |||||||| | || ||| |||||||
Db      430  TTTTGTACGGAACGAAAAGCCTGGGGGTCAATATCCCCGGGTCAAGCGGTTAATC   489

Qy      480  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC   539
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      490  TAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC   549

Qy      540  GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGCGGTTTTGTAAGTCAGATGTGAAATCCCCGG   599
             ||||||||||||||||||||||  ||| |||| |||||| |||| ||||||||||||||||
Db      550  GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTTTGTAAGACAGTGTGAAATCCCCGG   609

Qy      600  GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA   659
             ||||||||||||||||||| |||| ||| |||||||||||||||||||||||||||||||
Db      610  GCTCAACCTGGGAACTGCATTTGTGACTGCGCAGCTAGAGTAGGGGCAGAGGGGGATGGAA   669

Qy      660  TTCCATGTGTAGCGGTGAAATGCGTAGAGATATCGGAGGAACACCGATGGCGAAGGCAGCC   719
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db      670  TTCCGCGTGTAGCAGTGAAATGCGTAGATATATGCGAGGAACACCGATGGCGAAGGCAATC   729

Qy      720  CCCTGGGTTAACACTTGACGCTCATGCGAGAAAGCGTGGGGAGCAAACAGGATTAGATACC   779
             ||||||||  |||||||||||||||||||||||| |||||||||||||||||||||||||
Db      730  CCCTGGGCCTGCCACTGACGCTCATGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC   789

Qy      780  CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCCTTACTAGGCTTGTAAC   839
             ||||||||||||||||||||||||||||||| ||| ||| |  |||||||||||||||||
Db      790  CTGGTAGTCCACGCCCTAAACGATGTCAACTGGTTGTTGGGTCTTCTTAACTGACTCAGTAAC   849

Qy      840  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG   899
             |||||||||||||| ||||| ||| |||| |||||||||||||||||| ||||||||||
Db      850  GAAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGTTGAAACTCAAAGG   909

Qy      900  AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA   959
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db      910  AATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGTTTAATTCGATGCAACGCGAAAA   969


Qy      960  ACCTTACCTACCCTTGACATGTAGTAGGCAATATTTTAGAGATAAAATAGTG--CCTTCGGGA  1017
             |||||     |||||||||||| |||||||||||| ||||||||||  ||||    ||||||||
Db      970  ACCTTACCCACCTTTGACATGGCTGGAATTGCTTTTGGTGGTGTTTGTGCTCGAAAGAGA  1029

Qy     1018  ACGCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGT  1077
             |||||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||
Db     1030  ACCTGCACACAGGTGTCGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGT  1089

Qy     1078  CCCGCAACGAGCGCAACCCCTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAG  1137
             |||||||||||||||||||||||||| ||||||||||||  ||||||||||||||||||
Db     1090  CCCGCAACGAGCGCAACCCCTTGCCATTAGTTGCTA-CATTCAGTTGAGCACTCTAATGGG  1148

Qy     1138  ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGG  1197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1149  ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATAG  1208

Qy     1198  GTAGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAG  1257
             ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1209  GTGGGGCTACACACGTGCTACAATGGCGTGTACAAAGGGTTGCCAACCCGCGAGGGGGAG  1268

Qy     1258  CTAATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCTCGCAACTCGACTCCGTGAAGTC  1317
             ||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db     1269  CTAATCTCCATAAAGCCAGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTC  1328

Qy     1318  GGAATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTTACA  1377
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     1329  GGAATCGCTAGTAATCGTGGATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTTACA  1388

Qy     1378  CACCGCCCGTCACACCATGGGAGTGGTTTCACCAGAAGAAGCAGATAGTCTAACCGTAA-GA  1436
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     1389  CACCGCCCGTCACACCATGGGAGTGGGTTCTGCCAGAAGTAGGTAGCCTAACCGTAAGGA  1448

Qy     1437  GGGCGTTTGCCACGCGGAGATTCATGACTGG  1467
             |||||||| ||||||||||||||||||||||
Db     1449  GGGCGCTTACCACGCGGGGGTTCGTCGTCGACTGG  1479


RESULT 2
US-08-114-695A-7
; Sequence 7, Application US/08114695A
; Patent No. 5508193
; GENERAL INFORMATION:
;    APPLICANT: Mandelbaum, Raphael T.
;    APPLICANT: Wackett, Lawrence P.
;    TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
;    TITLE OF INVENTION: WATER
;    NUMBER OF SEQUENCES: 8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
;      STREET: 3500 IDS CENTER
;      CITY: MINNEAPOLIS
;      STATE: MN
;      COUNTRY: USA
;      ZIP: 55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/114,695A
;      FILING DATE: 31-AUG-1993
;      CLASSIFICATION: 435
;    ATTORNEY/AGENT INFORMATION:
;      NAME: MUETING, ANN M.
;      REGISTRATION NUMBER: 33,977
;      REFERENCE/DOCKET NUMBER: 600.268US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 612-339-0331
;      TELEFAX: 612-339-3061
;  INFORMATION FOR SEQ ID NO: 7:
;    SEQUENCE CHARACTERISTICS:
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;   LENGTH: 1536 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: rRNA
;   ORIGINAL SOURCE:
;     ORGANISM: Pseudomonas testosteroni
US-08-114-695A-7

Query Match        75.3%;  Score 1104;  DB 2;  Length 1536;
Best Local Similarity   69.7%;  Pred. No. 0;
Matches 1026;  Conservative 256;  Mismatches 180;  Indels 10;  Gaps 6;
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Qy      1 TTGATCATGGCTCAGATTGAACGCTGGCGGCAT-GCTTTACACATGCAAGTCGAACGGCA   59
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Db     13 UUGAUCCUGGCUCAGAUUGAACGCUGGCGGCANGCUUUACACAUGCAAGUCGAACGGUA   72

Qy     60 GCACGGGTGCTTGCACCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGT  119
          |||||| ||| ||:|| :||||||||||||||| |||||||||||||||:|||||||||||
Db     73 ACAGGUCUUCGGA----UGCUGACGAGUGGCGAACGGGUGAGUAAUACACUCGGAACGUGC  128

Qy    120 CCAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGA  179
          ||||| |||||||||||||||||||||| ||| |||||||||| :||||||| ||||||||
Db    129 CUAGUAGUGGGGGAUAACUACUCGAAAGAGUAUACCGCAUGAGAUCUACGGAUGA      188

Qy    180 AAGCAGGGGATCGAAAGACCCTTGTGCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGG  239
          ||||||| |||||||||||| :||||||||||:||||||||:|||||||||||||:|||||
Db    189 AAGCAGGGGACCUUCGGGCCUUGUGCUACUAGAGCGGCCGAUGGCAGAUUAGUUAGUUGUG  248

Qy    240 TGGGGTAAAGGCTCACCAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACA  299
          :||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    249 UGGGGUAAAGGCUCACCAAGGCGACGAUCUGUAGCUGGUCUGAGAGGACGACCAGCCACA  308

Qy    300 CTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAAT  359
          |||||||||||||||||||||| |||| |||||||||||||||||||||||: ||:|||
Db    309 CUGGGACUGAGACACGGCCCAGACUCCUACGGGAGGCAGCAGUGGGGAAUUUUGGACAAU  368

Qy    360 GGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCT  418
          ||||||||||||||||:||||||||||||||||||||||:| |:||||| ||||||| |
Db    369 GGGCGAAAGCCUUGAUCCAGCAAUGCCGCGUGAGUGAAGAAGGCCUUCGGGUUGUAAAACUG  428

Qy    419 CTTTCAGTCGAGAAGAAAAAGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGA  478
          |::: ||||| ||||||||||||||:|||:||||| |||| ||||:|||||||||||||||
Db    429 CUUUUGUACGGAACGAAAAGCCUGGGCUAAUAUCCCGGUAUGGGUACGACCGUACGACUAGA  488

Qy    479 AGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAAT  538
          |:||||:||| |||||||||||||||||||||||||||||||||||||||||||||: ||:
Db    489 AUAAGCACCGGCUAACUACGUGCCAGCAGCCGCGGUAAUACGUAGGGUGCAAGCGUUAAU  548

Qy    539 CGGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCG  598
          |||||||||:|||||||||||||||||||||||||||:|:||:||||||||||||||||||
Db    549 CGGAAUUACUGGGCGUAAAGCGUGCGCAGGCGGUUUUGUAAGACAGGUGUGAAAUCCCCG  608

Qy    599 GGCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTGTAGAGGGGGGTGGA   658
          ||:|||||||||||| ||:|| :||||:|||| |||||| || |: |||||||||||:||
Db    609 GGCUCAACCUGGGAACUGCCAUUGUGACUGCGAGGCUAGAGUGUUGGCAGAGGGGGGUAGA  668

Qy    659 ATTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGC  718
          ||:||:|| :||||||||||||||||||||||| ||| ||||| ||:|||||||||||||:
Db    669 AUUCCGCGUGUAGCAGUGAAAUGCGUAGAUAUGCGGAGGAACACCGAUGGCGAAGGCAGC  728

Qy    719 CCCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGAGCAAACAGATTAGATAC   778
          :|||:||||| ||| |||||| ||:||||| |||||||||||| |||||||| ||:|||
Db    729 CCCCUGGGUUAACACUGACGCUCAUGCACGAAAGCGUGGGGAGCAAACAGGAUUAGAUAC  788

Qy    779 CCTGGTAGTCCACGCCCTAAACGATGTCAACTAGCTGTTGGGCCTTACTAGGCTTGGTAA  838
          ||:||||||||||||||| ||:|| |:|:|||| |:|| :||||||:|||||| |||||||
Db    789 CCUGGUAGUCCACGCCCUAAACGAUGUCAACUAGCUGUUGGGGUCUUAACUGAUCUCAGUA  848

Qy    839 CGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAG  898
          ||||||||||||||:|| |||||||||||||||:||| ||| ||||||||||||:|:||||
Db    849 CGAAGCUAACGCGUGAAGUUGACCGCCUGGGGAGUACGGUCGCAAGAUUAAAACUCAAAG  908
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Qy    899 GAATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAA  958
          || ||||||||||||||||||:||||:||||||||||||||||||:||| :||||||||||
Db    909 GAAUUGACGGGGACCCGCACAAGCGGUGGAUGAUGUGGUUUAAUUCGAUGCAACGCGAAA  968

Qy    959 AACCTTACCTACCCTTGACATGTAGCGAATATTTTAGAGATAAAATAGTG--CCTTCGGG 1016
          ||:| ||| :|:||:||||| |||||||||||||:: ||:||::||||||||||::||:|
Db    969 AACCUUACCCACCUUUGACAUGGCAGGAACUUUCCAGAGAUGGAUUGGUGUUCGGCAGGAG 1028

Qy   1017 AACGCTAACACAGTGCTGCACGGCTGTCATGGCTGTCGTCGTCAGCTCGTGTCGTGAGATG 1076
          |||| |||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db   1029 AACUGCACAGGUGCUGCAUGGCUGUCGUCAGCUCGUGUCGUGAGAUGUUGGGUUAAG 1088

Qy   1077 TCCCGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTTAGTTGGGCACTTTAATGA 1136
          :|||||||||||||||||:||| || ||:|| ::|||:: :||:||:||:||| || |||
Db   1089 UCCCGCAACGAGCGCAACCCUUGUCAUUAGUUGCUA-CAUUCAGUUGGGCACUCUAAUGG 1147

Qy   1137 GACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCCTTATG 1196
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   1148 GACUGCCGGUGACAAACCGGAGGAAGGUGGGGAUGACGUCAAGUCCUCAUGGCCCUUAU   1207

Qy   1197 GGTAGGGCTTCACACGTAATACAATGGGCGCTACAGAGGGTTGCCAACCCGCGAGGGGGA 1256
          ||||||| |||||| |||| ||||||||||||||||| |||||| ||||||||||:||||
Db   1208 GGUAGGGGCUACACACGUGCUACAAUGGGCGUACAAAGGGUUGCCAACCCGCGAGGGGGA 1267

Qy   1257 GCTAATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGT 1316
          ||:||||| ||||||||| |:|| || |:| :|||||||||||||||||||||||||:|
Db   1268 GCUAAUCCCAUAAAGCGUAUCGUAGUCCGGAUCGUAGUCUGCAACUCGACUACGUGAAGU 1327

Qy   1317 CGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTAC 1376
          |||||:|||||||||||||:||||| :|||||||||||||||||||||||||:||:||||
Db   1328 CGGAAUCGCUAGUAAUCGUGGAUCAGCAUGCCACGGUGAAUACGUUCCCGGGUCUUGUAC 1387

Qy   1377 ACACCGCCCGTCACACCATGGGAGTGGGTTTCCAGAGAAGCAGCAGATAGTCTAACCGTAA-G 1435
          ||||||||||||||||||||:||:||:|||:|| || ||||:||| :|||:|||||||||| |
Db   1388 ACACCGCCCGUCACACCAUGGGAGUGGGUUGCACCAGAAGUAGCUAGUCUAACCGUAAGG   1447

Qy   1436 AGGGCGTTTGCCACGGCGAGATTCATGACTGG 1467
          |||||| ||||||||:|||||||| | |: ||:
Db   1448 AGGGCGCUUACCACGGCGGGGUUCGUGACUGG 1479
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RESULT 3
US-08-114-695A-8
; Sequence 8, Application US/08114695A
; Patent No. 5508193
; GENERAL INFORMATION:
;   APPLICANT: Mandelbaum, Raphael T.
;   APPLICANT: Wackett, Lawrence P.
;   TITLE OF INVENTION:  DEGRADATION OF S-TRIAZINES IN SOIL AND
;   TITLE OF INVENTION:  WATER
;   NUMBER OF SEQUENCES:  8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
;     STREET:  3500 IDS CENTER
;     CITY:  MINNEAPOLIS
;     STATE:  MN
;     COUNTRY:  USA
;     ZIP:  55402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/114,695A
;     FILING DATE:  31-AUG-1993
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  MUETING, ANN M.
;     REGISTRATION NUMBER:  33,977
;     REFERENCE/DOCKET NUMBER:  600.268US1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  612-339-0331
```

```
;  TELEFAX: 612-339-3061
;  INFORMATION FOR SEQ ID NO:  8:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 1474 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
;  MOLECULE TYPE: rRNA
;  ORIGINAL SOURCE:
;    ORGANISM: Pseudomonas cepacia
US-08-114-695A-8

Query Match    74.5%;  Score 1092.2;  DB 2;  Length 1474;
Best Local Similarity  68.3%;  Pred. No. 0;
Matches  996;  Conservative  252;  Mismatches  202;  Indels  9;  Gaps  4;

Qy     1  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGC-A    59
          :: :| ::|||||:  |||:: ||||||||||:||||:|||||||||||||||||||  |
Db    13  UUNAUUCCUGGCUCAGAUUNAACGCUGGCGGCAUGCCUUACACAUGCAAGUCGAACGGCNA    72

Qy    60  GCACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAGTCATCGGAACGTGT   119
          | ::|||||| ||  :|||||||||||||:||||||||||:|||||||||:|| |||||
Db    73  GCAUCGGGUGCUUNACCUGGUGGCGAGUGGCGGACGGGUGAGUAGUCAUCGGAACAUGU   132

Qy   120  CCAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCCATATTCTTCTACGGAGGA   179
          |||:|||||||||||:|||||:  | |||||| ||||||:||:|||||:: |:||||||||
Db   133  CCUGUAGUGGGGGAUAGCNCGGCGAAAGCNNAUUAUACCGCNNAUAUUCUUACGGAUGA   192

Qy   180  AAGCAGGGGATCGAAAGACCTTGTCTTTTGAGCGGCCGATGCCTGATTAGCTAGTTGG   239
          |||||||| |:|||||||||| ||: | ||| |||||:||:|||||||:|||:|||||
Db   193  AAGCGGGNGACCUUCGGGCCUCGCGUAUAGGGGUUGGCCUGAUUAGCUAGUUGG   252

Qy   240  TGGGGTAAAGGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACA   299
          |||||||||||:||||||||||||:||:|||  ||:||| :|||||||||||||||||||
Db   253  UGGGGUAAAGGCCUACCAAGGCGACGAUCAGUNGCUGGUCUGAGAGGACGACCAGCCACA   312

Qy   300  CTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAAT   359
          |||||||||||||||||| :||||:||||||||||||||||||||||||: ||||||||
Db   313  CUGGGACUGAGACACGGCCCNGACUCCUACGGGAGGCAGCAGUGGGGAAUUUUGGACAAU   372

Qy   360  GGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG--CTTCGGGTTGTAAAGCT   418
          ||||||||||||||:||||||||||||||||:||:|||||||  ||:|||||:|||||||
Db   373  GGGCGAAAGCCUGAUCCAGCAAUGCCGCGUGUGUGAAGAAGGCCUUCGGGUUGUAAAGCA   432

Qy   419  CTTTCAGTCGAGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGA   478
          | ::|   ||||||| |||||  ||  ||  ||| ::||:::||:|||||| |||| |:||
Db   433  CUUUUGUCCGGGAGAAGAAAUCCUGGCUCUAAUACAGCCGGGGAUGACGGUACCGGAAGA   492

Qy   479  AGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGGTGGGGGCAAGCGTTAAT   538
          |:|||||||||||:||||||:|:  |||||||||||:|| ||| :|:|||:|| :::| |
Db   493  AUAAGCACCGGCUAACUACGUGCCAGCAGCCGCGGNNNAUACCGUAGGGUGCAAGCGUUAAU   552

Qy   539  CGGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCG   598
          ||||||||| ||||||||||||:|||||||||:||:  | |||||||||||||||||||:
Db   553  CGGAAUUACUGGGCGUAAAGCGUGCGCAGGCGGUUUGUUAAGUCUGAUGUGAAAUCCCCG   612

Qy   599  GGCTTAACCTGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGA   658
          |||||||||:|||||  :|: | |:|||||||| |||| ||:||||| |||||||::||
Db   613  GGCUCAACCUGGGACUGCAUUCGAAACUGGCAGGCUAGAGUAUGGNNAGAGGGGGGUAGA   672

Qy   659  ATTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGC   718
          |::||||| || |||||||||:||||||||||||||||||| | |||||:||||||||||
Db   673  AUUCCACGUGUAGCAGUGAAAUGCGUAGAGAUAUGGAAGAACAUCGAUGGCGAAGGCAGC   732

Qy   719  CCCTGGTGGTTTAAACTGACGCTCATGCGACGAAAGCGTGGGGAGCAAACAGGATTAGATAC   778
          ||| ||| | :: |:|||||:|:|||||:||:|||||| :|||||||||| ||:||||||||
Db   733  CCCUGGGGCCGAAACUGACGCUCAUGCGACGAAAGCGUGGGGAGCAAACAGGAUUAGAUAC   792

Qy   779  CCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGGCTTGGTTAA   838
          |||::|||||||:|:  |: ::|||| ||| ||   |::||| :: |||| |
Db   793  CCUGGUAGUCCACGCCCUAAACGAUGUCAACUAGUUGUUGGGGCAUUUCCUUAGUAA   852

Qy   839  CGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAAG   898
          ||||:|:|||||:|||| |:||| |:|||||||||||||| :||||||||||||||||||
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Db   853  CGUAGCUAACGCGUGAAGUUGACCGCCUGGGGAGUACGGUCGCAAGAUUAAAACUCAAAG   912

Qy   899  GAATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTGATGCAACGCGAAA   958
          |||||||||||||||| |||||||||:|||| ||||| || |||||:||||||||||||
Db   913  GAAUUGACGGGGACCCGCACAAGCGGUGGAUUAUGUGGAUUAAUUCGAUGNAACGCGAAA   972

Qy   959  AACCTTACCTACCCTTGACATGTAGCGAATATTTAGAGATAAAATAGTG--CCTTCGGG   1016
          ||:|: :| ||||| |||||| :  |||||||   ||| | :|| | |:  |||||||||
Db   973  AACCUUACCUACCCUUGACAUGGCAGAAUCCUGCUGAAAGCUGGGAGUGCCUCGCAAAGAG   1032

Qy  1017  AACGCTAACACAGTGCTGCATGCTGCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAG   1076
          |||||: || ||||||:|||||||||:||||||||||||||||||||: |||:||:||
Db  1033  AACCGGCGCACAGGUGCUGCAUGGCUGUCGUCAGCUCGUGUCGUGAGAUGUUGGGUUAAG   1092

Qy  1077  TCCCGCCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTTAGTTGGGCACTTTAATGA   1136
          |||||:|||||||||:|||||:  | |      :||| ||: | |:||||||:|  |||::
Db  1093  UCCCGCAACGAGCGCAACCCUUGUCAUUAAUUGCC----UAGCGCANAGAGCACUCUAAUGA   1147

Qy  1137  GACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATG   1196
          |||:||:|||||||| |||||||:|||:|||||||||| |||||||:|||||||| |||:
Db  1148  GACUGCCGGUGACAAACCGGAGGAAGGUGGGGAUGACGUCAAGUCCUCAUGGCCCUUAUG   1207

Qy  1197  GGTAGGGCTTCACGTAATACAATGGCGCTACAGAGGGTTGCCAACCCGCGAGGGGGA   1256
          ||:|||||||||| ||| |:|:|||||:  | |||||||:||||||||||||||||||
Db  1208  GGUAGGGCUUCACACGUCGGAACAAUGGCGCAUACAGUCGGAACAGAGGGUUGCCAACCCGCGAGGGGGA   1267

Qy  1257  GCTAATCTCAGAAAGCCGTCGTAGTCCGGATCAGCAGTTCGCAACTGCAGCAGAAGC   1316
          || ||| :||| ||| |:||:|| |||||||||||:||:|||| |||||:|||||||
Db  1268  GCUAAUCCCAGAAAACCGAUCGUAGUCCGGAUCGCAGUCGGUGCAACUCGACUGCAUGAAGC   1327

Qy  1317  CGGAATGCGTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTAC   1376
          |||||| |||||||||||| || |||||||||||||||||| |||:||||||:|||| ||
Db  1328  UGGAAUCGCUAGUAAUCGCGGAUCAGCAUGCCGCGGUGAAUACGUUCCCGGGUCUUGUAC   1387

Qy  1377  ACACCGCCCGTCACACCATGGGAGTGGGTTGCTTAACCGTTAACCGTAAGA   1436
          |||||||||||||||||||||| | |||||||:||:  :||| |||||||
Db  1388  ACACCGCCCGUCACACCAUGGGAGUGGGUUGCUUAACCGAAGUUAACCGUAAGGGGGG   1447

Qy  1437  GGGCGTTTGCCACGGCGAG   1455
          ||||||:||:|||:|||||
Db  1448  AGGANNGUCACNANGGUAG   1466
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RESULT 4
US-09-726-774-5
;  Sequence 5, Application US/09726774
;  Patent No. 6677153
;  GENERAL INFORMATION:
;    APPLICANT: Iversen, Patrick L.
;    TITLE OF INVENTION: Antisense Antibacterial Method and
;    TITLE OF INVENTION: Composition
;    FILE REFERENCE: 0450-0032.30
;    CURRENT APPLICATION NUMBER: US/09/726,774
;    CURRENT FILING DATE: 2000-11-29
;    PRIOR APPLICATION NUMBER: US 60/168,150
;    PRIOR FILING DATE: 1999-11-29
;    NUMBER OF SEQ ID NOS: 139
;    SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 5
;    LENGTH: 1544
;    TYPE: DNA
;    ORGANISM: Neisseria gonorrhoea
US-09-726-774-5

Query Match    74.3%;  Score 1090.4;  DB 3;  Length 1544;
Best Local Similarity  85.5%;  Pred. No. 0;
Matches 1261;  Conservative   0;  Mismatches 206;  Indels  7;  Gaps  4;

Qy     1  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG    60
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    14  TTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG    73
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Qy    61  CACGGGTGCTTGCAC----CTGGTGGCGAGTGGCGACGCGGGTGAGTAATGCATCGGAACG  116
          |||  | |||||||||    ||||||||||||||||| |||||||||||| ||||||||||
Db    74  CACAGGGAAGCTTGCTTCTCGGGTGGCGAGTGGCGAACGGGTGAGTGAGTAACATCGGAACG  133

Qy   117  TGTCCAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGA   176
          | ||| | |||| ||||||||| |  |||||||| | |||||||||||||||||||||||
Db   134  TACCGGGTAGCGGGGGGATAACTAGTCGAAAGATCAGCTAATACCGCATAACGTCTTGAGAG  193

Qy   177  GGAAAGCAGGGGATCGAAAGACCTTGTCGTTTGGGAGCGGCCGATGCCTGATTAGCTAGT   236
          ||||||||||||  | |||||||||||| ||  ||||||||| || ||||||||||||| |
Db   194  GGAAAGCAGGGGACCTTCGGGCCTTGCGCTATCCGAGCGGCCGATATCTGATTAGCTGGT   253

Qy   237  TGGTGGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCC   296
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254  TGGCGGGGTAAAGGCCCACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCC   313

Qy   297  ACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGAC   356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314  ACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGAC   373

Qy   357  AATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAA   415
          ||||||||  |||||||||||||||||||||||| | |||||||| ||||||||||||||
Db   374  AATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAA   433

Qy   416  GCTCTTTCAGTCTGAGAGAAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGAC   475
          |  ||||  | |  ||| |||||||   |  | || ||| |  |  |||||  ||||| ||
Db   434  GGACTTTTGTCAGGGAAGAAAAAGGCTGTTGTTGCCAATATCGGCCCGATGACGTACCTGA   493

Qy   476  AGAAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTT   535
          |||| |||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   494  AGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTT   553

Qy   536  AATCGGAATTACTGGGCGTAAAGGGTGCGCAGGCGGTTTGTAAGTCAGATGTGAAATCC   595
          ||||||||||||||||||||||| ||||||||| |||| | |||| ||||||||||||||
Db   554  AATCGGAATTACTGGGCGTAAAGCGGGCGCAGACGGTTACTTAAGCAGGATGTGAAATCC   613

Qy   596  CCGGGCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGT   655
          ||||||| |||| ||||| ||||||  ||||   | ||| |||||||| ||||||| |||
Db   614  CCGGGCTCAACCCGGGAACTGCGTTCTGAACTGGCGGGTCGAGTGTGTCAGAGGGAGGT   673

Qy   656  GGAATTCCATGTGTAGCAGTGAAATGCGTAGAGATCGTGAAGGAACATCGATGGCGAAGGC   715
          |||||||||| |||||||||||||||||||||||||||| |||||  | ||||||||||||
Db   674  GGAATTCCACGTGTAGCAGTGAAATGCGTAGAGATCGTGGAGGAATACCGATGGCGAAGGC   733

Qy   716  AGCCCCCTGGGTTAACACTGACGCTCATGCAGCGAAAGCGTGGGGAGCAAACAGGATTAGA   775
          |||| ||||| |||||||||||| |||||   |||||||||||| |||||||||||||||
Db   734  AGCCTCCTGGGATAACACTGACGTTCATGTCCGAAAGCGTGGGTAGCAAACAGGATTAGA   793

Qy   776  TACCCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGG--CTTACTAGGCTTG   834
          |||||||||||||||||||| ||||||||||||||||||||||||  |||| |  |||||
Db   794  TACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCAACTTGATTGCTTG   853

Qy   835  GTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTC   894
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854  GTAGCGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTC   913

Qy   895  AAAGGAATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGC   954
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914  AAAGGAATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGC   973

Qy   955  GAAAAACCTTACCTACCCTTGACATGGTCTGAGAATATTTAGAGATAAAATAGTGCCTTCG   1014
          ||| ||||||||||   ||||||||| | |||| ||  ||| |||| ||| ||||||||||
Db   974  GAAGAACCTTACCTGGTCTTGACATGTCGTTGACCGCCTGGAGACAGGTGTTTCCCTTCG   1033

Qy  1015  GGAACAGCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTA   1074
          |||  || |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1034  GGAGCAGAGTGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTA   1093

Qy  1075  AGTCCCGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTAAGTTGGGCACTCTTAAT   1134
          ||||||||||||||||||||||| ||| ||| |||||||||||  |||||||||||| | 
Db  1094  AGTCCCGCAACGAGCGCAACCCTCGTCCTTAGTTGCCATCATTCAGTTGGGCACTCTAAG   1153

Qy  1135  GAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTA   1194
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  1154  GAGACTGCCGGTGACAAGCCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTA   1213

Qy  1195  TGGGTAGGGCTTCACACGTAATACAATGGCGCCTACAGAGGGTTGCCAACCCGCGAGGGG   1254
          ||  ||||||||||||||| |||||||| |  |||||||||| |||||| ||||||| |
Db  1214  TGACCAGGGCTTCACACGTCATACAATGGTCGGTACAGAGGGTAGCCAAGCCGCGAGGCG   1273

Qy  1255  GAGCTAATCTCAGAAAGCGGCGTCGTAGTCCGATCGCAGTCTGCAACTCGACTCCGTGAA   1314
          ||||  ||||||  ||  | | |||||||||| | ||| ||||||||||||| | | ||||
Db  1274  GAGCCAATCTCACAAAACCGATCGTAGTCCGGATTGCACTCTGCAACTCGAGTGCATGAA   1333

Qy  1315  GTCGGAATCGCTAGTAATCGCCGGATCGCATGCCGCGGTGAATACGTTCCCGGGTCTTGT   1374
          |||||||||||||||||||||| ||  ||||| ||||||||||||||||||||||||||||
Db  1334  GTCGGAATCGCTAGTAATCGCAGGTCAGCATACTGCGGTGAATACGTTCCCGGGTCTTGT   1393

Qy  1375  ACACACCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA   1434
          |||||| |||||||||||||||||||||  | |||||||| || |||| ||||||||
Db  1394  ACACACCGCCCGTCACACCATGGGAGTGGGGATACCAGAAGTAGGTAGGGTAACCGCAA   1453

Qy  1435  -GAGGGGCGTTTGGCCACGGCGACGATTCATGACTGG   1467
            ||| ||  ||| ||||||  |  ||||||||||||
Db  1454  GGAGTCCGCTTACCACGGTATGCTTCATGACTGG   1487
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Query Match      73.9%;  Score 1084.8;  DB 3;  Length 1453;
Best Local Similarity 86.3%;  Pred. No. 0;
Matches 1260;  Conservative 0;  Mismatches 187;  Indels 13;  Gaps 5;
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Qy    12  TCAGATGAACGCTGGCGGCGTGCTTTACACATGCAAGTCGAACGTGAACGGCCGGGTGCTT   71
          ||||||  | |||| || | |  ||||||||| || ||| ||||||| |||| ||| |||
Db  1453  TCAGATTGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAACGTGAACATGCAGCGCGGG----G   1398

Qy    72  GCACCTGGTGCGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGG   131
          ||||||||| ||| ||||||||||||||||||||||  | ||||||||| |||  | ||||
Db  1397  CAACCTGGTGCGGCGAGTGGCGGACGGGTGAGTAACACATCGGAACGTGGGG----G   1338

Qy   132  GATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGGAGCAGGGGATC   191
          |||||||||||| ||||  | |||||||||||| | ||||||  |||||||||||
Db  1337  GATAGCCCCGGAAAGCGGGGAATCGCCGGAGGAGTGAAGAAGTGGGGGACC   1278

Qy   192  GAAAGACCTTGTCGTTTGGGAGCGGCCGATGCTCGATGAGTGGGTAAAGC   251
          || | | || |||| ||||||||||||||| ||  |  ||||| |||||||
Db  1277  GCAAGGCCTCACGCGTTGGTGAGGCGGCCGATGGCAGATTAGGTAGTTGGTGGGGTAAAGC   1218

Qy   252  CTACCAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA   311
          || ||||||||||||||  | |||  | ||||||||  | |  ||  |  |||||||||||
Db  1217  TTACCAAGCCTGCGATCTGTAGCTGGTCTGCGAGGATGATCAGCCACACTGGGACTGAGA   1158

Qy   312  CACGGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT   371
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Db    82  ACACCATGGGAGCGGGGTTCTGCCAGAAGTAGTAGTTAGCCTAACCGCAAGGAGGGCGATTACC  23
              |||||
Qy  1448  ACGGGCAGATTCATGACTGG  1467
              ||||| ||||
Db    22  ACGGCAGGTTCGTGACTGG  3
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RESULT 6
US-08-642-229A-3
; Sequence 3, Application US/08642229A
; Patent No. 5874291
GENERAL INFORMATION:
 ; APPLICANT: Herwig, Russell P.
 ; APPLICANT: Bieleeldt, Angela R.
 ; APPLICANT: Stensel, H. David
 ; APPLICANT: Strand, Stuart E.
 ; TITLE OF INVENTION: Degradation of Environmental Toxins by a
 ; TITLE OF INVENTION: Filamentous Bacterium
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Christensen O'Connor Johnson and Kindness PLLC
 ; STREET: 1420 Fifth Avenue, Suite 2800
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: WA 98101-2347
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/642,229A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/246,865
 ; FILING DATE: 20-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sheiness, Diana K.
 ; REGISTRATION NUMBER: 35,356
 ; REFERENCE/DOCKET NUMBER: UOFW19233
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 682 8100
 ; TELEFAX: (206) 224 0779
 ; TELEX: 4938023
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1455 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: nucleic acid
 ; DESCRIPTION: "16S ribosomal DNA"
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Unknown. Possibly new species
 ; STRAIN: A-1
US-08-642-229A-3

Query Match   73.7%;   Score 1081.6;   DB 2;   Length 1455;
Best Local Similarity 86.6%;   Pred. No. 0;
Matches 1262;   Conservative 1;   Mismatches 182;   Indels 13;   Gaps 6;

Qy   16 ATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTCGAC 75
             |||||||||||||||||||||||||||| ||||||||||||| ||||||
Db   1 ATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAGCGCAGCATGG--GCTTCGGC 58

Qy   76 CTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA 135
             |||||||||||||||||||||||
Db   59 CTGATGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACGGTGTCCTGTAGTGGGGGATA 118
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Db  1157  CACGGCGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCT  1098
              |||||||||||||||
Qy   372  GATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAG  430
              |||||  ||||||||
Db  1097  GATCCAGCCATTCCGCGTGCAGGACGAAGGCCTTCGGGTTGTAAACTGCTTTGTACGGA  1038

Qy   431  AAGAAAGGTTGTGACTAATAATCACAACTTATGATGACGTACCGACAGAAGAAGCACCGGC  490
              ||||||||||| ||| ||||
Db  1037  ACGAAAGGGCTCTCTCTAATACAGGGGCGATATGACGGTACCGTAGAATAAGCACCGGC  978

Qy   491  TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG  550
              ||||||||||||||||||||
Db   977  TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG  918

Qy   551  GCGTAAAGGGTGCGCAGGCGGCTTGTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGG  610
              ||||||| ||||||||||||||
Db   917  GCGTAAAGCGTGCGCAGGCGGTTTGTTAAGACAGAGGGGTGGAATTCCCGGGCTCAACCTGG  858

Qy   611  GAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAATTCCATGTGTA  670
              |||||  ||||  |||
Db   857  GAACTGCCTTTGTGACTGCAAGGCTGGAGTGCGGCAGAGGGGGATGGAATTCCCGCGTGTA  798

Qy   671  GCAGTGAAATGCGTAGAGATATGCGGAGGAACATCGATGGCGAAGGCAGCCCCTGGGGTTAA  730
              ||||||||||| |||  |||
Db   797  GCAGTGAAATGCGTAGATATATGCGGAGGAACACCGGTGGCGAAGGCAATCCCCTGGGCCTG  738

Qy   731  CACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA  790
              |||||||||||||||||||||||||
Db   737  CACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA  678

Qy   791  CGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGTAGCTAACGC  850
              ||||||||||||||||||
Db   677  CGCCCTAAACGATGTCAACTGGTTGTTGGGAATTCATTTTCTCAGTAACGAAGCTAACGC  618

Qy   851  GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG  910
              ||||||||||||||||||||
Db   617  GTGAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAAGGAATTGACGGGG  558

Qy   911  ACCCGCACAAGCGGTGGATGATGTGGTTTAATTCGATGCAACGCGAAAAACCTTACCTAC  970
              ||||||||||||||||| ||
Db   557  ACCCGCACAAGCGGTGGATGATGTGGTTTAATTCGATGCAACGCGAAAAACCTTACCCAC  498

Qy   971  CCTTGACATGTAGCGAATATTTTAGAGATAAATAGTG--CCTTCGGGAACGCGCTAACACA  1028
              ||||||||||||||||||
Db   497  TTTTGACATGTACGGAATCCTGCTGAAAGCAGGAGAGTGCTGAAAGAGAGGCGCTAACACA  438

Qy  1029  GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG  1088
              |||||||||||||||||
Db   437  GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG  378

Qy  1089  CGCAACCCTTGTCATCATCATCTGCCATCATTAGTTGGGACTTTAATGAGACTGCCGGTGA  1148
              ||||||||||
Db   377  CGCAACCCTTGCCATTAGTTGCTACGA-----AAGGGCACTCTAATGGGACTGCCGGTGA  323

Qy  1149  CAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTATGGGTAGGGGCTTCA  1208
              ||||||||||||||||||
Db   322  CAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTATAGGTGGGGCTACA  263

Qy  1209  CACGTAATACAAATGGCGCGTACAGAGGGCTGCCAACCCGCGAGGGGGAGCTAATCTCAGA  1268
              ||||| |||||||||
Db   262  CACGTCATACAAATGGCTGGTACAAAGGGTTGCCAACCCGCGAGGGGGAGCCAATCGCTAG  203

Qy  1269  AAGCCGCTCGTAGTCCGGATCGCAGTCTGCAACTCCGGTCGAAGTCGGAATCGCTAG  1328
              |||||  ||||||||||||||||
Db   202  AAGCCAGTCGTAGTCCGGATCGCAGTCTCGAACTCGACTCGGAAGTCGGAATCGCTAG  143

Qy  1329  TAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC  1388
              ||||||  |||||||||
Db   142  TAATCGTGGATCAGCATGCCACGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC  83

Qy  1389  ACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCC  1447
              |||  |||
Db  1389  ACACCATGGGAGCGGGGTTCTGCCAGAAGTAGTAGTTAGCCTAACCGCAAGGAGGGCGATTACC  1447
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RESULT 7
US-09-342-579-1
; Sequence 1, Application US/09342579
; Patent No. 6187569
; GENERAL INFORMATION:
; APPLICANT: BRAMUCCI, MICHAEL G.
; APPLICANT: MCCUTCHEN, CAROL M.
; APPLICANT: NAGARAJAN, VASANTHA
; APPLICANT: THOMAS, STUART M.
; TITLE OF INVENTION: Microbial Production of Terephthalic Acid and
; TITLE OF INVENTION: Isophthalic Acid
; FILE REFERENCE: CL-1257
; CURRENT APPLICATION NUMBER: US/09/342,579
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/091,645
; EARLIER FILING DATE: JULY 2, 1998
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Burkholderia sp.
US-09-342-579-1

Query Match   73.5%;   Score 1078.2;   DB 3;   Length 1451;
Best Local Similarity   86.0%;   Pred. No. 0;
Matches 1243;   Mismatches   193;   Conservative   0;   Indels   9;   Gaps   4;

Db   1445 ACTGG 1449

RESULT 8
US-09-617-854A-1
; Sequence 1, Application US/09617854A
; Patent No. 6461840
; GENERAL INFORMATION:
;   APPLICANT: BRAMUCCI, MICHAEL G.
;   APPLICANT: MCCUTCHEN, CAROL M.
;   APPLICANT: NAGARAJAN, VASANTHA
;   APPLICANT: THOMAS, STUART M.
;   TITLE OF INVENTION: Microbial Production of Terephthalic Acid and
;   TITLE OF INVENTION: Isophthalic Acid
;   FILE REFERENCE: CL-1257
;   CURRENT APPLICATION NUMBER: US/09/617,854A
;   CURRENT FILING DATE: 2001-09-04
;   PRIOR APPLICATION NUMBER: 60/091,645
;   PRIOR FILING DATE: JULY 2, 1998
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
;   LENGTH: 1451
;   TYPE: DNA
;   ORGANISM: Burkholderia sp.
US-09-617-854A-1

Query Match   73.5%;   Score 1078.2;   DB 3;   Length 1451;
Best Local Similarity   86.0%;   Pred. No. 0;
Matches 1243;   Conservative   0;   Mismatches   193;   Indels   9;   Gaps   4;

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Qy      26 GGCGGCATGCTTTACACATGCAAGTCGAACGCAGCAGACGGGTGCTTGCACCTGGTGGCGA   85
           ||||||||||| || |||||||||||||||||| |||||||  |||||||||||||||||
Db      11 GGCGGCATGCCTTACACATGCAAGTCGAACGAATTCAAACGCGACAGCAGCGGGTGCTTGCACCTGGTGGCGCGA  70

Qy      86 GTGGGACGACGGGTGAGTAATGCGTAATGGAATTCATGGAAGCTGTCCAGAAGTGGGGGATAACGCATCGAA  145
           ||| ||||||||||||||||||||||| | |||||||||||| |||||||| | ||| || |
Db      71 TTGGGCAACGGGTGAGTAATACATCGGAATGTAATCATCGGAATGTGAGTGGGGGGATAACCTCGGGCAAA  130

Qy     146 AGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAAGACCTTGTGC  205
           ||||||||| ||||||||| | || |||||||||||| |||| || |||| | |  ||
Db     131 AGCCGGATTAATACCGGCATACGTCCTGAGGAGGAAAGCGGGGGAACCTTCGGGCCTCGCGC  190

Qy     206 TTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAGGCAACG  265
           ||| ||||||  ||||| ||| |||||||||||||| ||| |||||||||||||||||| |
Db     191 TACAAAGCAGCGACGATGTCAAATTACCTATTTGGTGGGGTAAAAGGCCTCACCAAGGGCGACA  250

Qy     266 ATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTC  325
           ||| |||||||| |||||||||||| |||||| ||||||| ||||||||||||| |||||
Db     251 ATCTGTACCTGGTCTGAGAGGACGACCAACCACACTGGGACTGAGACACGGCCCAAACTC  310

Qy     326 CTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGCGAAAGCCTGATCGCAGCAATGCC  385
           |||||||||||||||||||||||||| || ||||||||||||| |||| ||||||||||
Db     311 CTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCGCAGCAATGCC  370

Qy     386 GCGTGAGTGAAGAAGG--CTTCGGGTGTGTAAAGCTCTTTCAGTCGGGAAGAAAGGTTGTG  444
           |||||||||||||| |  | ||||||||||||| |||||| ||  || ||||| |||||
Db     371 GCGTGTGTGAAGAAGGCCTTCGGGTTGTGTAAAGCACTTTTGTTCCGGAAGAAATCCTCTGG  430

Qy     445 ACTAATAATCACAACTTATGATGGTACCGGACAGAGAAGCACCGGCTAACTACGTGCCAG  504
           |||| ||||||||||||| ||| || |||| |||||||| |||||||||||| ||||||
Db     431 GTTAATACCTCGGGGGATGACGGTACCGGGGATGACGGTTAATACCTCGGGGGATGACGG  489

Qy     505 CAGCCGCGGTAATACGTAGGGTCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCG  564
           ||||||||||||||||| |||||||||||||||||| |||||| ||||||||||||| ||
Db     490 CAGCCGCGGTAATACTTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCG  549

Qy     565 CAGGCGGCTTTGTAAGTCAGATGTGAAATCCCGGGGCTTAACCTGGGAATTGCGTTTGAA  624
           |||||||||| |||| ||| |||||||||||||||| ||||||||||||||||||||||
Db     550 CAGGCGCGTTTTGTAAGACGGATGTGAAATCCCGGGGCTTAACCTGGGAACTGCATTCGTG  609

Qy     625 ACTACAAAGCTAGAGTGTAGCAGAGGGGGTGAATTCCATGTGTAGCAGTGAAATGCGT  684
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     371 GCGTGTGTGAAGAAGGCCTTCGGGTTGTGTAAAGCACTTTTGTTCCGGAAGAAATCCTCTGG  430

Qy     445 ACTAATAATCACAACTTATGATGGTACCGGACAGAGAAGCACCGGCTAACTACGTGCCAG  504
           |||| |||||||| |||| ||| || |||| |||||||| |||||||||| | |||||
Db     431 GTTAATACCTCGGGGGATGACGGTACCGGGGATGACGGTTAATACCTCGGGGGATGACGG  489

Qy     505 CAGCCGCGGTAATACGTAGGGTCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCG  564
           ||||||||||||||||| |||||||||||||||||| ||||||| ||||||||  | ||
Db     490 CAGCCGCGGTAATACTTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCG  549

Qy     565 CAGGCGGCTTTGTAAGTCAGATGTGAAATCCCGGGGCTTAACCTGGGAATTGCGTTTGAA  624
           |||||||| |||||| ||| |||||||||||||||| ||||||||||| | || ||
Db     550 CAGGCGCGTTTTGTAAGACGGTAGCCTAACCGGTAAGGGCGCTTACCCAGGGGGGTGAATTCG  609

Qy     685 AGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACTGACGCTCATG  744
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     670 AGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCCCATGGGTTAACACTGACGCTCATG  729

Qy     745 CACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTGAAGTTGACCGC  804
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     730 CACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTGAAGTTGACCGC  789

Qy     805 TCAACTAGTTGTTGGGCCTTACTAGGCTTGGTTGACTAGCTAACGCTGAAGTTGACCGC  864
           ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db     849 TCAACTAGTTGTTGGGATTCATTTCTTAGTAACGAAGCTAACGCGTGAAGTTGACCGC  793
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(alignment continues)

Db   1463 ACTGG 1467

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             STREET:  1420 Fifth Avenue, Suite 2800
             CITY:  Seattle
             STATE:  Washington
             COUNTRY:  USA
             ZIP:  WA 98101-2347
          COMPUTER READABLE FORM:
             MEDIUM TYPE:  Floppy disk
             COMPUTER:  IBM PC compatible
             OPERATING SYSTEM:  PC-DOS/MS-DOS
             SOFTWARE:  PatentIn Release #1.0, Version #1.30
          CURRENT APPLICATION DATA:
             APPLICATION NUMBER:  US/08/642,229A
             FILING DATE:
             CLASSIFICATION:  435
          PRIOR APPLICATION DATA:
             APPLICATION NUMBER:  US 08/246,865
             FILING DATE:  20-MAY-1994
          ATTORNEY/AGENT INFORMATION:
             NAME:  Sheiness, Diana K.
             REGISTRATION NUMBER:  35,356
             REFERENCE/DOCKET NUMBER:  UOFW19233
          TELECOMMUNICATION INFORMATION:
             TELEPHONE:  (206) 682 8100
             TELEFAX:  (206) 224 0779
             TELEX:  4938023
    INFORMATION FOR SEQ ID NO: 2:
          SEQUENCE CHARACTERISTICS:
             LENGTH:  1452 base pairs
             TYPE:  nucleic acid
             STRANDEDNESS:  single
             TOPOLOGY:  linear
          MOLECULE TYPE:  nucleic acid
             DESCRIPTION:  "16S ribosomal DNA"
          HYPOTHETICAL:  NO
          ANTI-SENSE:  NO
          ORIGINAL SOURCE:
             ORGANISM:  Brachymonas denitrificans AS-P1
US-08-642-229A-2

Query Match      72.7%;    Score 1066.8;    DB 2;    Length 1452;
Best Local Similarity  85.6%;    Pred. No. 0;
Matches 1247;   Conservative   0;   Mismatches  197;   Indels  12;   Gaps   5;

Qy   16  ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTGCAC   75
         |||||||||||||||||||||| ||||||||||||||||||||||||||||||   |||||
Db    1  ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGGTAACAGT---CCTTCGG   57

Qy   76  CTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAAGGGTGCTTCAGAAGTGGGGGATA  135
         ||||  |||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   58  ATGCTGACGAGTGGCGAACGGGTGAGTAATGTATCGGAAGGGTGCTTCAGAAGTGGGGGATA  117

Qy  136  ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA   195
         || |||||||||| || ||||||||||| |||  |  ||| ||  || | |||| ||||
Db  118  ACTACTCGAAAGAGTGGCTAATACCGCGATATCAGAGGAGAACTGAGGTTGGTGGGGTAAAGGCCTTG  177

Qy  196  GACCTTGTGCTTTTGGAGGCGGCCGATGGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC   255
         |||||||||| ||||||||| |||||||||| |||| |||||||||||||||||| |||||||
Db  178  GGCCTCGCGCTACTGGACGCGGCGGCCGATATCAGATTAGCTAGTTGGTGGGGTAAAGGCCTAC   237

Qy  256  CAAGGCAACGATCAGTAGTTGGTGCTGAGGACGACCAGCCACACTGGGACTGAGACACACG   315
         ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  238  CAAGCCCAGATCGTTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACACG   297

Qy  316  GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC   375
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  298  GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC   357

Qy  376  CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGTTGTAAAGCTCTTTCAGTCGAGAAGA   434
         |||||||| ||||||| ||| ||||| |||||||||||| |||||||||||  |||||| |
Db  358  CAGCAATGCCGCGTGCAGGAAGGAGGCCTTCGGGTTGTAAACTGCTTTTGTTACAGAACCGA   417

Qy  435  AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAGAAGCACCGGCTAAC   494
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Db  610  ACTGCAAGGCTAGAGTATGGCGAGAGGGGGTAGAATTCCACGTGTAGCAGTGAAATGCGT   669
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Qy  685  AGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACTGACGCTCATG   744
         |||||| ||||  |||| |||||||||||||||||||||||||   |||||||||||||||
Db  670  AGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAATACTGACGCTCATG   729

Qy  745  CACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATG   804
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  730  CACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATG   789

Qy  805  TCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGTAGCTAACGCGTGAAGTTGACCGC   864
         ||||||||||||||||| ||| |     | ||||||  |||||||||||||||||||||||
Db  790  TCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGAAGCTAACGCGTGAAGTTGACCGC   849

Qy  865  CTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGG   924
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Db  850  CTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGG   909

Qy  925  TGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGTAGC   984
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  910  TGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGTACG   969

Qy  985  GAATATT--TTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCTGCATGGCT  1042
         ||||  ||    ||||| | |  ||  |||  | || |   ||||||||||||||||||||
Db  970  GAATCTTGCTGAGAGGTGAGAGTGCTCGAAAGAGAACCGTAACACAGGTGCTGCATGGCT  1029

Qy 1043  GTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCA  1102
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db 1030  GTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCC  1089

Qy 1103  TTAATTGCCATCATTTAGTTGGGACACTTAATGAGACTGCCGGTGACAAACCGGAGGAAG  1162
         |||  |||| | |    ||     ||||| | | ||||||||||||||||||||||||||
Db 1090  TTAGTTGCCTACGCAA------GAGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAG  1144

Qy 1163  GTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTAATACAATG  1222
         ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| ||
Db 1145  GTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTCATACACATG  1204

Qy 1223  GCGCGGGACAGAGGGTTGCCAACCCCGAGAGGGGAGCTAATCTCAGAAAAGCCGCGTCGTAGT  1282
         | ||| |||||||||| |||||| | |||||  |||||||  | |||||| |||| |||||||
Db 1205  GTCGTACAGAGGGCTGCCAAACCGGCGAGGTGGAGCTAACCCAGAAAACCGATCGTAGT  1264

Qy 1283  CCGGATCGGAGTCTGCGAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCGCGGATCAG  1342
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Db 1265  CCGGATCGCGAGTCTGCGAACTCGACTCGTGAAGTCGGAATCGCTAGTAATCGCGGATCAG  1324

Qy 1343  CATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTG  1402
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Db 1325  CATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTG  1384

Qy 1403  GGTTTCACCGAAGCAGATAGTCTAACCGTAAGGGGGCGTTTGCCACGGCGGAGATTCATG  1462
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Db 1385  GGTTTTGCCAGAAGTAGGTAGCCTAACCGTAAGGGGAGGGGCCTTACCACGGCTGGATCATG  1444

Qy 1463  ACTGG  1467
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Db 1445  ACTGG  1449
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RESULT 9
US-08-642-229A-2
; Sequence 2, Application US/08642229A
; Patent No. 5874291
; GENERAL INFORMATION:
; APPLICANT: Herwig, Russell P.
; APPLICANT: Bielefeldt, Angela R.
; APPLICANT: Stensel, H. David
; APPLICANT: Strand, Stuart E.
; TITLE OF INVENTION: Degradation of Environmental Toxins by a
; TITLE OF INVENTION: Filamentous Bacterium
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson and Kindness PLLC

```
; Sequence 1, Application US/09063898
; Patent No. 6319497
; GENERAL INFORMATION:
;   APPLICANT: Casida, Jr., Lester E.
;   APPLICANT: Falkinham, III, Joseph Oliver
;   APPLICANT: Cain, Cody C.
;   TITLE OF INVENTION: NON-OBLIGATE PREDATORY BACTERIUM
;   TITLE OF INVENTION: BURKHOLDERIA CASIDAE AND USES THEREOF
;   NUMBER OF SEQUENCES: 1
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds LLP
;     STREET: 1667 K Street, N.W.
;     CITY: Washington
;     STATE: DC
;     COUNTRY: USA
;     ZIP: 20006
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/063,898
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/044,532
;     FILING DATE: 23-APR-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Misrock, Leslie
;     REGISTRATION NUMBER: 18,872
;     REFERENCE/DOCKET NUMBER: 8743-006-999
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212)79090090
;     TELEFAX: (212)8697941
;     TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1495 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: unknown
;     TOPOLOGY: unknown
;   MOLECULE TYPE: Genomic DNA
US-09-063-898-1

Query Match             71.9%;  Score 1054.6;  DB 3;  Length 1495;
Best Local Similarity   86.7%;  Pred. No. 0;
Matches 1267;  Conservative 0;  Mismatches 179;  Indels 15;  Gaps 9;

Qy    14 AGATTGAACGCTGGCGGCAGTGCTTACA-CATGCAAGTCGAACGGCAGCACCGGTGCTTG  72
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Db     1 AAATATTTACGTCGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACCGGTGCTTG  60

Qy    73 CACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAAC-GTGTCCAGAAGTGGGG 131
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Db    61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTCGGG 120

Qy   132 GATAACCGTCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGAAAAGCAGGGGATC 191
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Db   121 GATAGCCGGCGGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAAGCGGGGGACC 180

Qy   192 GAAAGACCTTGTCGTTTTGGAGCGGCCGATGCCGATTAGTAGTTGGTGGGGTAAAGGC 251
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Db   181 TTCGGGCCTCGCGCGATTAGATAGGGTGGCCGATGCCGATTAGCTAGTTGGTGGGGTAAAGGC 240

Qy   252 CTACCAAGGCAACGATCAGTAGTTGT-GTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 311
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Db   241 CTACCAAGGCGACGATCAGTAGTT-GTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 299

Qy   312 CACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 371
         |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   300 CACGGCCCAGACTCCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 359

Db   418 AAAGGCTCTCGTTAATACCTGGGGCTCATGACGGTACTGTAAGAGAATAAGCACCGGCTAAC 477

Qy   495 TACGTTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   478 TACGTTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGGTTAATCGGAATTACTGGGCGT 537

Db   555 AAAGGCGTGCGCAGGCGGCCGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 614
Qy   538 AAAGGCGTGCGCAGGCGGTTTGTGTAAGACCGATGTGAAATCCCCGGGCTCAACCTGGGAAC 597

Qy   615 TGCGTTGAAACTACAAAGCTAGAGTGTGAGAGAGGGGGGTGGAATTCCATGTGTAGCAG 674
         ||| ||| |  ||||| |||||||||| | ||||||||| ||||||||| ||||||||
Db   598 TGCATTGGTGGTGACTGCAAGGCTGGAGTGCGGCAGAGGGGGGATGGAATTCCGCGTGTAGCAG 657

Qy   675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGGCGAAGGCAGCCCCCTGGGTAACACT 734
         ||||||||||||||||||| ||||||||||||| ||||||||  || |||||| ||  |
Db   658 TGAAATGCGTAGATATGTGGAGGAACACCGATGGCGAAGGCAATCCCCTGGGCCTGCACT 717

Qy   735 GACGCTCATGCACGAAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGTCCACGCC 794
         |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   718 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGTCCACGCC 777

Qy   795 CTAAACGATGTCAACTAGTTGTTGGGGCCTTACTAGGCTTGGTAACGTAGCTAACGCGTGA 854
         |||||||||||||||||||||| ||||  || ||| | |||| |||||||||||||||||
Db   778 CTAAACGATGTCAACTGGTTGTTGCTTACTCAGTAACGAAGCTAACGCGTGA 837

Qy   855 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 914
         ||||||||||| |||||||||||||||| ||||||||||||||| |||||||||||||||
Db   838 AGTTGACCGCCCGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 897

Qy   915 GCACAACGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 974
         ||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||||
Db   898 GCACAACGCGGTGGATGTCGTTTAATTCGATGCAACGCGAAAAACCTTACCCACCCTTT 957

Qy   975 GACATGTAGCGAATATTTTAGAGATAAAATAGTG---CCTTCGGGAACGCTAACACAGGTG 1032
         |||||| || |||   |  ||||||||| |    |||| |||| ||||| |||||||||||
Db   958 GACATGCAGCAGAATTCCGAAGAGATTGGGAGTGCTCGTCGTAAGAGACTGCCGTAGACAGGTG 1017

Qy  1033 CTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1092
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1018 CTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1077

Qy  1093 ACCCTTGTCATTAATTGCCATCATCATTTAGTTGGGCACTCTAATGGGACTGCCGGTGACAAA 1152
         |||||| ||||||| ||||||||||||| || ||   ||| ||| |||| |||||||||||
Db  1078 ACCCTTGTCATTAGTTGCTAATGGGCACTCTACGA-----AAGGGACTCTAATGGGACTGCCGGTGACAAA 1132

Qy  1153 CCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGTGTAGGGCTTCACACG 1212
         |||||||||||||||||||||||||||||||||| |||||  | |||||| ||| ||||||
Db  1133 CCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATAGGTGGGGCTACACACG 1192

Qy  1213 TAATACAATGGGCGCGTACAGAGGGCTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGC 1272
         | |||| |||||||| ||||||| | | ||||||||| |||||||||||||| ||||||||
Db  1193 TCATACAATGGGCGCGTACAAAGGGTAGCCAACCCGCGAGGGGGAGCCAATCCCATAAAGC 1252

Qy  1273 GCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAAT 1332
         || |||||||| |||||||| ||||||||||| |||||||||||||||| || |||| ||
Db  1253 CGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAAT 1312

Qy  1333 CGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACAC 1392
         |||||||||||| || |||||||||||||||| ||||||||||||||||||||||||||||
Db  1313 CGTGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACAC 1372

Qy  1393 CATGGGAGTGGGTTTCACCAGAAGCAGCAGATAGTGTTAGCCTAACCGTAA-GAGGGCCACGG 1451
         |||||||||||| |||| || ||||||||||| |||||| ||||||| ||||||||||||||
Db  1373 CATGGGAGCGGGTTCTGCCAGAAGTAGCAGATAGTGTTAGCCTAACCGTTAGGAGGGCCACGG 1432

Qy  1452 CGAGATTCATGACTGG 1467
         |||| ||||||||||
Db  1433 CAGGGTTCGTGACTGG 1448
```

Db   1433 CACGGTAGGATTCATGACTGG 1453

RESULT 11
US-09-985-846-1
; Sequence 1, Application US/09985846
; Patent No. 6689357
; GENERAL INFORMATION:
;   APPLICANT: Casida, Jr., Lester E.
;   Falkinham, III, Joseph Oliver
;   Cain, Cody C.
;   TITLE OF INVENTION: NON-OBLIGATE PREDATORY BACTERIUM
;   BURKHOLDERIA CASIDAE AND USES THEREOF
;   NUMBER OF SEQUENCES:1
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds LLP
;   STREET: 1667 K Street, N.W.
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20006
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/985,846
;   FILING DATE: 06-No. 6689357-2001
;   CLASSIFICATION: <unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/063,898
;   FILING DATE: 22-APR-1998
;   APPLICATION NUMBER: 60/044,532
;   FILING DATE: 23-APR-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Misrock, Leslie
;   REGISTRATION NUMBER: 18,872
;   REFERENCE/DOCKET NUMBER: 8743-006-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)7909090
;   TELEFAX: (212)8699741
;   TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1495 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: unknown
;   TOPOLOGY: unknown
;   MOLECULE TYPE: Genomic DNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-985-846-1

Query Match   71.9%;   Score 1054.6;   DB 3;   Length 1495;
Best Local Similarity 86.7%;   Pred. No. 0;
Matches 1267; Conservative   0; Mismatches 179; Indels 15; Gaps 9;

Qy   14 AGATTGAACGCTGGCGGCAGTGCTTACA-CATGCAAGTCGAACGGCAGCGGCACGGGCTG 72
           |||||||||||||||||||||||||||| ||||||||||||||| |||| ||||||||||||
Db   1 AAATATTAGCGTGGTTGCATGCCTTACAGCAGTGCAAGTCGAACGGCAGCGGCACGGGCTTG 60

Qy   73 CACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAAC-GTGTCCAGAAGTGGGG 131
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   61 CACCTGGTGGCGAGTGGCGGACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120

Qy   132 GATAACCGATCGAAAGATGTGCTAATACCGCATATTCTACGGAAGAGGGGATC 191
           |||||||||||||||||||||||||| |||||||||||||||||||||||
Db   121 GATAGCCCCGACGAAAGCGGGATTAATACCGCATACGATCTACGGAAGAAAGCGGGGGACC 180

Qy   192 GAAAGACCTTGTGCTTTTGGAGCGGCCGATGCCGATGAGTTGGTCGTAGTTGGTAAGGC 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTCGGGCCTCGGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240

Qy   1447 CACGGCGAGATTCATGACTGG 1467

Qy   1329 TAATCGGATCAGCATGCTGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC 1388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 TAATCGGATCAGCATGCTGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTC 1372

Qy   1389 ACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAAG--AGGGCGTTGC 1446
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   1373 ACACCATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCC 1432

Qy   1447 CACGGCCGAGATTCATGACTGG 1467
          ||||||||||||||||||||||
Db   1433 CACGGTAGGATTCATGACTGG 1453

RESULT 12
US-09-735-567-2/c
; Sequence 2, Application US/09735567
; Patent No. 6608190
; GENERAL INFORMATION:
;   APPLICANT: Bramucci, Michael
;   TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
;   TITLE OF INVENTION: Industrial Wastewater Bioreactors
;   FILE REFERENCE: BC1033 US NA
;   CURRENT APPLICATION NUMBER: US/09/735,567
;   CURRENT FILING DATE: 2000-12-13
;   PRIOR APPLICATION NUMBER: 60/171,140
;   PRIOR FILING DATE: 16 DECEMBER 1999
;   NUMBER OF SEQ ID NOS: 30
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
;   LENGTH: 1467
;   TYPE: DNA
;   ORGANISM: Unknown Organism
; FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Brachymonas
;   OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain NBYB13
US-09-735-567-2

Query Match   71.5%; Score 1049.2; DB 3; Length 1467;
Best Local Similarity   85.2%; Pred. No. 0;
Matches 1244; Conservative   0; Mismatches   203; Indels   13; Gaps   6;

Qy   14 AGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCACGGGTGCTTGC 73
          |||||||||||||||||||||||||||||||||||||||||||| || ||||||||
Db   1467 AGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAG--CCGCTCCTTCG 1410

Qy   74 ACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGA 133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 GGATGGCGGAGTGGCGGACGGGTGAGTAATGCATCGGAACATCGGAACGTGCCCGGTAGTGCCGGGA 1350

Qy   134 TAACGCATCGAAAGATGTGCTAATACCGCATATTCCTACGGAGGAAAGCAGGGGA--TC 191
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||| ||
Db   1349 TAGTCTGGGAAAGCCGGATTAATACCGCATAATCCGTGATTAGTAGTTGGTGGGGACTCG 1290

Qy   192 GAAAGACCTTGTCTTTTGGAGCGGCCGATGCGGCCGGGCCGGTAAGGC 251
          |||||||||||||||||||||||||||||||||||||| ||||||||
Db   1289 CAAGGGCCCTTGCGCTACTGGAGCGGCCGATGTCGATTAGGTAGTTGGTGGGGTAAAGGC 1230

Qy   252 CTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 311
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1229 CCACCAAGGCGACTGCCAGCTGGAGTCTGTGAGGAGGATGATCAGCCACACTGGGACTGAGA 1170

Qy   312 CACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 371
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   1169 CACGGCCCGAACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCT 1110

Qy   372 GATCCAGCCAATGCCGCGTGTACGGAAGAAGG--CTTCGGGTTGTAAAGCTCTTTCAGTCGAG 430
          ||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||||||
Db   1109 GATCCAGCCAATGCCGCGTGCAGGATGAAGGCCTTCGGGTTGTAAACTGCTTTTGTACGGA 1050

Qy   431 AAGAAAGGTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGC 490
          ||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Db   1049 ACGAAAGGGCGTCTTTCTAATAAAGAGGGCACATGACGTACCGTACCGTGAAGAATCGCTAG 990

; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; TITLE OF INVENTION: Industrial Wastewater Bioreactors
; FILE REFERENCE: BC1033 US NA
; CURRENT APPLICATION NUMBER: US/09/735,567
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/171,140
; PRIOR FILING DATE: 16 DECEMBER 1999
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
;
SEQ ID NO 6
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Brachymonas
; OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain RA6
US-09-735-567-6

Query Match   71.5%;   Score 1048.4;   DB 3;   Length 1539;
Best Local Similarity 85.3%;   Pred. No. 0;
Matches 1242;   Conservative 0;   Mismatches 201;   Indels 13;   Gaps 6;

Qy   18 TGAAGCTGGCGGCGATGCTTACACATGCAAGTCGAACGGCAGCAGCGGGTGCTTGCACCT   77
           ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   1538 TGAAGCTGGCGGCGATGCTTACACATGCAAGTCGAACGGCAGCGC--GTCCTTCGGGAT 1481

Qy   78 GGTGGCCAGTGGCGACGGGTGAGTAATGCATCGGAACGTGTCCAGAGTGGGGGATAAC   137
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 GGCGGCGAGTGGCGAACGGGTGAGTAAAGCATCGGAACGTGCCCGGTAGTGCGGGATAGC 1421

Qy   138 GCATCGAAAGATGTCTAATAACCGCATATTCTTACGGAGAAGAAGCAGGGGATC--GAAA   195
           ||||||||||||||| |||||||||||||||||||||||||||||||||||||| ||||
Db   1420 TCGGCGAAAGCCGGATTAATACCGCATGAGATCCGATGAGAAGCAGGGGACCCGCAAG 1361

Qy   196 GACCTTGTCTTTGGAGCGGGCCGATGCCGATGGAGTAGTTGGTGGGGTAAAGGCTAC   255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 GGCCTTGCGGCTACTACGGGTGTCTGAGCGGATGATCAGCCACATCGGGACTGAGACACG 1301

Qy   256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG   315
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   1300 CAAGCCTCGATCTGTAGCTGGTCTGAGAGGACGATCAGCCACATCGGGACTGAGACACG 1241

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGCAGTGGGAATTTTGGACAATGGGCGAAAGCCTGATC   375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 GCCCGAACTCCTACGGGAGGCAGCAGCAGTGGGAATTTTGGACAATGGGCGCAAGCCTGATC 1181

Qy   376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA   434
           ||||| |||||||||||||||||||| || ||||||||||||||||| |||||||||||||
Db   1180 CAGCCATGCCGCGTGCAGGATGAAGGCCTTCGGGTTGTAAACTGCTTTGTACGGACGAACGA 1121

Qy   435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACGGACAGAAGAAGCACCGGCTAAC   494
           ||||||| |||||||| |||||| || ||| ||| ||||| |||||||||||||||||
Db   1120 AAGGGCTCTTTCAATAAAGAGGCACACTGAGGGTCACCGTAAGATAAGCACCGGCTAAC 1061

Qy   495 TACGTGCCAGCAGCCGCGGTAATACGGTGGGGGCAAGCGTTAATCGGAATTACTGGGCGT   554
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 TACGTGCCAGCAGCCGCGGTAATACGGTGGGGGCGAGCGTTAATCGGAATTACTGGGCGT 1001

Qy   555 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAAT   614
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1000 AAAGCGTGCGCAGGCGGCTCTTGCAAGACCAGTGTGTGAAATCCCCGGGCTCAACCTGGGAAC   941

Qy   615 TGCGTTTGAAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAATTCCATGTGTAGCAG   674
           || |||||||||||||||||| |||||||||||||||||||||| ||||||||||||||
Db   940 TGCCATTGTGACTGCAAGGCTGGAGTACGGCAGAGGGGGATGGAATTCCGCGTGTAGCAG   881

Qy   675 TGAAATGCGTAGAGATATGGAAGAACATCGATGCGAAGGCAGCCCCCTGGGTTAACACT   734
           ||||| |||||||||||||||||||||||||| |||||||||||||||||||||| ||||
Db   880 TGAAATGCGTAGATATGCGGAGGAACACCGATGGCGAAGGCAGCCCCCTGGGCCTGTACT   821

Qy   735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC   794

Qy   491 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG   550
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   989 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGG   930

Qy   551 GCGTAAAGGGTGCGCAGGCGGCTGGTAAGTCGAAGATGTGAAATCCCCGGGCTTAACCTGG   610
           ||||| |||||||||||||||||||| |||| ||| ||||||||||||||||||||||||
Db   929 GCGTAAAGCGTGCGCAGGCGGCAGCACAGTGGTGAAATCCCCGGGCTCAACCTGG   870

Qy   611 GAATTGCGGTTTGAAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGAATTCCATGTGTA   670
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   869 GAACTGCCATTGTGACTGCAAGGCTGGAGTACGGCAGAGGGGGGATGAATTCCGCGTGTA   810

Qy   671 GCAGTGAAATGCGGTAGAGATATGCGGAGGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAA   730
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   809 GCAGTGAAATGCGTAGATATGCGGAGGAACATCGATGGCGAAGGCAGCCCCCTGGGTTCA   750

Qy   731 CACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA   790
           ||||||||| |||||||||||||||||||||||||||||| |||||||||||||||||||
Db   749 TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA   690

Qy   791 CGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGTAGCTAACGC   850
           |||||||||||||||||||||||||||||| ||| |||| |||||||||||||||||||||
Db   689 CGCCCTAAACGATGTCAACTGGTTGTTGGGGATTTATTCTTCAGTAACGAAGCTAACGC   630

Qy   851 GTGAAGTTGACCGCCTGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG   910
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   629 GTGAAGTTGACCGCCTGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG   570

Qy   911 ACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC   970
           |||||||||||||||||||| ||| |||||| |||||||||||||||||||||||||||||
Db   569 ACCCGCACAAGCGGTGGATGTGGTTTAATTCGATGCAACGCGAAAAACCTTACCCAC   510

Qy   971 CCTTGACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTC--GGGAACGCTAACACA 1028
           |||||||| ||| |||||| ||||||| ||||||||||||| |||||||||||||||
Db   509 CTTTGACATGTATGGGAATCCCGCAGAGATGCGGGAGTGCTCGCAAAGAGAGCCATAACACA   450

Qy   1029 GGTGCTGCATGGCTGTCGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG 1088
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   449 GGTGCTGCATGGCTGTCGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG   390

Qy   1089 CGCAACCCTTGTTCATTAGTTGCCATCATTTAGTTGGGCACTTTAATGAGACTGCCGGTGA 1148
           |||||||||||||||||| ||||||||||| |||||||||||||||||| |||||||||
Db   389 CGCAACCCTTGTCGATCGTTGCTAGCTGGTTCGATGGGCACTCTGATCGGACTGCCGGTGA   335

Qy   1149 CAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGGCTTCA 1208
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   334 CAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATAGGTGGGGCTACA   275

Qy   1209 CACGTAATACAATGGCCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGA 1268
           |||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   274 CACGTCATACAATGGCCGGTACAAAGGGTTGCCAACCCGCGAGGGGGAGCCAATCCCATA   215

Qy   1269 AAGGCGGTCGTAGTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAG 1328
           |||||| |||||||||| ||||| |||||||||||||||||||| ||| ||||||||||||
Db   214 AAGGGCTCGTAGTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAG   155

Qy   1329 TAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC 1388
           |||||||||||||||| ||| |||||||||||||||||||||||||||||||||||||||
Db   154 TAATCGTGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC   95

Qy   1389 ACACCATGGGAGTGGGTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGGCGTTTGCC 1447
           |||||||||||||||||||||||| ||||||||| |||||||||| ||||| |||||||
Db   94 ACACCATGGGAGTGGGTTCTCCAGAAGCAGGTAGCCTAACCGCAAGGGGGGCGCTTACC   35

Qy   1448 ACGGCCGAGATTCATGACTGG 1467
           |||||||||||||| ||||||
Db   34 ACGGTGGGGTTCGTGACTGG   15

RESULT 13
US-09-735-567-6/c
; Sequence 6, Application US/09735567
; Patent No. 6608190

; OTHER INFORMATION: Nucleotide sequence of the 16S rDNA corresponding to strain RA9
US-09-735-567-7

Query Match   71.4%;   Score 1047.8;   DB 3;   Length 1454;
Best Local Similarity   85.2%;   Pred. No. 0;
Matches 1242; Conservative   0; Mismatches 202; Indels 13; Gaps 6;

```
Qy     17  TTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGCAGCACGGGTGCTTGCACC  76
               ||||||||||||||||||||||||||||||||||||||||||||||   |||||||
Db      1  TTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGCAGCACGGC--GTCCTTCGGGA  58

Qy     77  TGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATAA  136
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     59  TGGCGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGCCCGTGTCGTGGGGGATAG  118

Qy    137  CGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGA--TCGAA  194
               |||||||||||||||||||||||||||||||||||||||||||||
Db    119  CTCGGGCGAAAGCCCGGATTAATACCGCATGAGATCCGTGATGAAAGCAGGGGACTCGCAA  178

Qy    195  AGACCTTGTCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTA  254
               |||||||||||||||||||||||||||||||||||||||||||||||
Db    179  GGGCCTACTGCGCTACTGCGCTGCGATAGTTAGTTGGTGGGGTAAAGGCCCA  238

Qy    255  CCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACAC  314
               |||||||||||||||||||||||||||||||||||||||||||
Db    239  CCAAGCCTGCGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACATCGGGACTGAGACAC  298

Qy    315  GGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGAT  374
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Db    299  GGCCCGAACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGAT  358

Qy    375  CCAGCAATGCCGCGTGAGTGAAGAAG--CTTCGGGTTGTGTAAAGCTCTTTCAGTCGGAAG  433
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Db    359  CCAGCCATGCCGCGTGCAGGATGAAGGCCTTCGGGTTGTAAACTGCTTTTGTACGGAACG  418

Qy    434  AAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAA  493
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Db    419  AAAGGGTCTTTCTAATAAAGAGGGACACAATGACGTACCGTAGAATAAGCACCGGCTAA  478

Qy    494  CTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCG  553
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Db    479  CTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCG  538

Qy    554  TAAAGGGTGCGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAA  613
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Db    539  TAAAGCGTGCGCAGGCGGTTCTGCAAGACGGTGGTGAAATCCCCGGGCTCAACCTGGGAA  598

Qy    614  TTGCGTTGAAACTACAAAGCTAGAGTGTGTCAGAGGAGGGGTGGAATTCCATGTGTAGCA  673
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Db    599  CTGCCATTGTGACTGCAAGGCTGGAGTACGGCAGAGGGGGATGGAATTCCGCGTGTAGCA  658

Qy    674  GTGAAATGCGTAGAGATATGGAGGAAGACATCGATGGCGAAGGCAGCCCCCTGGGTTAACAC  733
               |||||||||||||||||||||||||||||||||||||||||||||
Db    659  GTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCCCCCTGGGCCTGTAC  718

Qy    734  TGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGTCCACGC  793
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Db    719  TGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGC  778

Qy    794  CCTAAACGATGTCAACTAGTTGTTGGGGATTCATTAGGCTTGGTCGTAGCTAACGCGTG  853
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Db    779  CCTAAACGATGTCAACTGGTTGTTGGGGATTTATTTCTTCAGTAACGAAGCTAACGCGTG  838

Qy    854  AAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACC  913
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Db    839  AAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACC  898

Qy    914  CGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCT  973
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Db    899  CGCACAAGCGGTGGATGATGTGGTTTAATTCGATGCAACGCGAAAAACCTTACCCACCTT  958

Qy    974  TGACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTC--GGGAACGCTACAACAGGT  1031
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(Left column continued)

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Db    820  GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  761

Qy    795  CTAAACGATGTCAACTAGTTGTTGGGGCCTTCGGGCCTTAGGCTTGGTAACGCGTGA  854
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Gb    760  CTAAACGATGTCAACTGGTTGTTGGGGATTTATTTCTTCAGTAACGAAGCTAACGCGTGA  701

Qy    855  AGTTGACCGCCTGGGGAGTACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGACCC  914
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Qy    915  GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  974
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Db    580  GACATGTATGAGAGATGTGGGAGTGCTCGCAAGAGAGCCATAACACAGGTG  521

Qy   1033  CTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA  1092
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Db    520  CTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA  461

Qy   1093  ACCCTTGTCATTAATTGCCATCATCATTTAGTTGGGCACTCTTAATGAGACTGCCGGTGACAAA  1152
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Db    460  ACCCTTGCCATCAGTTGCTACGAAA------GGGCACTCTGATGGGACTGCCGGTGACAAA  406

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Qy   1213  TAATACAATGGCCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGC  1272
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Qy   1273  GGCTCGTAGTCGGATCCGGATCTGACTTCGGTAGTCCGTAGTAAT  1332
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Qy   1333  CGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCGTCACAC  1392
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Db    225  CGTGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACAC  166

Qy   1393  CATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA--GAGGGCCTTTGCCACCG  1451
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Db    165  CATGGGAGTGGGTTGCTCCAGAAGCAGGTAGCCTAACCGCAAGGGGGCGGCGCTTGCCACGG  106

Qy   1452  CGAGATTCATGACTGG  1467
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Db    105  TGGGGTTCGTGACTGG  90
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RESULT 14
US-09-735-567-7
; Sequence 7, Application US/09735567
; Patent No. 6608190
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; TITLE OF INVENTION: Industrial Wastewater Bioreactors
; FILE REFERENCE: BC1033 US NA
; CURRENT APPLICATION NUMBER: US/09/735,567
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/171,140
; PRIOR FILING DATE: 16 DECEMBER 1999
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Brachymonas

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Db    959  TGACATGTATGGAATCCCCAGAGAGTGTGGGAGTGCTCCAAGAGAGCCATAACACAGT 1018
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Qy   1032  GCTGCATGGCTGCTCGTCGTCGTCGTGCGTGAGATGTTGGGTTGGCT 1091

Qy   1019  GCTGCATGGCTGCTCGTCGTCGTCGTGCGTGAGATGTTGGGTTGGCT 1078

Db    129  TGCCCAGTCGTCGTGGGGGATAACATAGGAGAGTGCTAATACCGCATACGACCTACGGG 188

Qy    177  GGAAAGCAGGGGATCGAAAGACCTTGTCGTTTTGGAGCGGCCGATGCCTGATTAGCTAGT 236
           |||||||||||||||||||||||| |||||||||| ||||||||||| ||||||||||||
Db    189  TGAAAGCGGGGGATCGGGGATGGTCGTCGTGAGAT 248

Qy    237  TGGTGGGGTAAAGGCCTACCAAGGCAACGATCAGTTGGTCTGAGAGACGACCAGCC 296
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Db    249  TGGCGGGGTAATGGCCCACCAAGGCGACGATCGGTAGCTGGTCTGAGAGGATGATCAGCC 308

Qy    297  ACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGAC 356
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Db    309  ACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGAC 368

Qy    357  AATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG--CTTCGGGTTGTAAA 415
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Qy    416  GCTCTTTCAGTCGGAGGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGTACCGAC 475
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Db    429  GCCCTTTGTCCGGAAGAAGAAAGCACTGGATTAATACTTCGGTGTTCTGACGTTACCGGA 488

Qy    476  AGAAGAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTT 535
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489  AGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTT 548

Qy    536  AATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCC 595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549  ACTCGGAATTACTGGGCGTAAAGCGTGCGTAGGCGGTTCGTTAAGTCTGATGTGAAAGCC 608

Qy    596  CCGGGCTTAACCTGGGAATTGCGTTGAAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGT 655
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Db    609  CTGGGCTCAACCTGGGAATTGCATTGAGTACTGGCGGGCTAGAGTGCGGTAGAGGATGGC 668

Qy    656  GGAATTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGC 715
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Qy    716  AGCCCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAACAGGATTAGA 775
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Qy    776  TACCCTGGTAGTCCAAACGATGTCAACTAGTTGTTGGGCCTTACTAGG--CTT 833
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Qy    834  GGTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGAGTACGGTCGCAAGATTAAAACT 893
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Db    849  AGTATCGAAGCTAACGCGTTAAGTTCGCCGCCTGGGGAGTACGGTCGCAAGACTGAAACT 908

Qy    894  CAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGTTTAATTCGATGCAACG 953
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Db    909  CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACG 968

Qy    954  CGAAAAACCTTACCTACCCTTGACATGTGACATGAAATATTTAGAGATAAAATAGTGCCTTC 1013
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Db    969  CGAAGAACCTTACCTGCCTTGACATGCACAGGAACTTTCCAGAGATGGATTGGTGCCTTC 1028

Qy   1014  GGGAACGCTAACACAGTGCTGCATGGCTGTCGTCGTCGTGCGTGTGGGTT 1073
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Db   1089  AAGTCCCGCAACGAGCGCAACCCTTGTCCCTAGTTGCCAGCACGTAATGGTGGGAACTCT 1148

Qy   1132  AATGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCC 1191
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Db   1149  AGGGAGACCGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCC 1208

Qy   1192  TTATGGGTAGGGCTTCACACGTGCTAATAACAATGGCCGCGTACAGAGGGTTGCCAACCCGCGAG 1251
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Db   1209  TTACGGCCAGGGCTACACACGTGCTACAATGGTCGGGACAGAGGGCTGCAAACTCGCGAG 1268
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RESULT 15

US-09-228-184-1

; Sequence 1, Application US/09228184
; Patent No. 6322782
; GENERAL INFORMATION:
; APPLICANT: WALKER, Harrell L.
; APPLICANT: HIGGINBOTHAM, Lawrence R.
; TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
; FILE REFERENCE: 013243-0007
; CURRENT APPLICATION NUMBER: US/09/228,184
; CURRENT FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 1540
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Bacterium SG-3;
; OTHER INFORMATION: gram negative; rod-shaped; exhibits flagellate
; OTHER INFORMATION: motility; pathogenic to cyanobacteria and algae;
; OTHER INFORMATION: yellow colonies on BG-11 medium suppl. with tryptic
US-09-228-184-1

Query Match   70.8%; Score 1037.6; DB 3; Length 1540;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 1243; Conservative   0; Mismatches 224; Indels   11; Gaps   6;

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Qy     61  CACGGGGTG----CTTGCACCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACG 116
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Db     69  CACAGCAGTAGCAATACTGTGTGGTGGCGAGTGGCGGACGGGTGAGGAATACATCGGAATC 128

Qy    117  TGTCCAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGA 176
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Qy     1252 GGGGAGCTAATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGT 1311
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Qy     1371 TTGTACACACCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACC 1430
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Qy     1431 GTAA-GAGGGCGTTTGCCACGGCGAGATTCATGACTGG 1467
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Job time : 304 secs

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                    GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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Searched:        5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters:    11766282

Minimum DB seq length:  0
Maximum DB seq length:  2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 4: gb_om:*
                 5: gb_ov:*
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                14: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1421.2	96.9	1450	1	AF272420	AF272420 Nitrosomo	
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31	1299.4	88.6	1470	1	AF272422	AF272422 Nitrosomo	
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37	1271.6	86.7	1497	1	AY123806	AY123806 Nitrososp	
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39	1269.8	86.6	1469	3	AF386755	AF386755 Nitrososp	
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ALIGNMENTS

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LOCUS       CQ796925               1467 bp    DNA        linear   PAT 19-APR-2004
DEFINITION  Sequence 18 from Patent WO2004026772.
ACCESSION   CQ796925
VERSION     CQ796925.1  GI:46408551
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Hovanec,T.A.
  TITLE     Ammonia-oxidizing bacteria and methods of using and detecting
            thesame
  JOURNAL   Patent: WO 2004026772-A 18 01-APR-2004;
            Aquaria Inc. (US)
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="N. Aestuarii-like AOB P4clone42 16S rDNA"
ORIGIN

Query Match             100.0%;  Score 1467;  DB 6;  Length 1467;
Best Local Similarity   100.0%;  Pred. No.2.8e-18;
Matches 1467;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db      1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG 60

Qy     61 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGGTGTC 120
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Db     61 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGGTGTC 120

Qy    121 CAGAAGTGGGGGATAACCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGAAGTGGGGGATAACCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA 180

Qy    181 AGCAGGGGGATCGAAAGACCCTTGCTTTTGGAGCGGCGCCGATGCCTGATTAGTTAGTTGGT 240
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Db   1261 ATCTCAGAAAGGCGGTCGTAGTCCGGATCGGAGTCGGAGTCTCGCAACTCGACTCCGTGAAGTCGGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321 ATCGCTAGTAATCGCGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACAC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATCGCTAGTAATCGCGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACAC 1380
Qy   1381 CGCCCGTCACCACCATGGGAGTGGTTTCACCAGAAGCAGATAGTCTAACCGTAAGAGGGC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGCCCGTCACCACCATGGGAGTGGTTTCACCAGAAGCAGATAGTCTAACCGTAAGAGGGC 1440
Qy   1441 GTTTGCCACGGCGAGATTCATGACTCG 1467
          |||||||||||||||||||||||||||
Db   1441 GTTTGCCACGGCGAGATTCATGACTCG 1467
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RESULT 2
AF386746
LOCUS   AF386746   1487 bp   DNA   linear   ENV 10-MAY-2004
DEFINITION Nitrosomonas sp. BF16c57 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF386746
VERSION   AF386746.1 GI:17864823
KEYWORDS   ENV.
SOURCE   Nitrosomonas sp. BF16c57
  ORGANISM Nitrosomonas sp. BF16c57
            Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
            Nitrosomonadaceae; Nitrosomonas; environmental samples.
REFERENCE   1 (bases 1 to 1487)
  AUTHORS   Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
  TITLE   Identification of bacteria responsible for ammonia oxidation in
            freshwater aquaria
  JOURNAL   Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
   PUBMED   11722936
REFERENCE   2 (bases 1 to 1487)
  AUTHORS   Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
  TITLE   Direct Submission
  JOURNAL   Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria
            Group, 6100 Condor Dr, Moorpark, CA 93021, USA
FEATURES   Location/Qualifiers
     source   1..1487
                     /organism="Nitrosomonas sp. BF16c57"
                     /mol_type="genomic DNA"
                     /isolation_source="ammonia-oxidizing bacteria isolated
                     from freshwater aquaria enrichments"
                     /db_xref="taxon:180505"
                     /clone="BF16c57"
                     /environmental_sample
     rRNA   <1..>1487
                     /product="16S ribosomal RNA"

ORIGIN

Query Match   98.2%;   Score 1440.2;   DB 3;   Length 1487;
Best Local Similarity 99.7%;   Pred. No. 7.9e-18;
Matches 1464;   Conservative   0;   Mismatches   3;   Indels   2;   Gaps   2;

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Qy      1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCGCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCGCAG 62
Qy     61 CACGGGTGCTTGCACCTGGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGGTGTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 CACGGGTGCTTGCACCTGGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGGTGTC 122
Qy    121 CAGAAGTGGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGACGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 CAGAAGTGGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGACGAA 182
Qy    181 AGCAGGGGATCGAAAGACCTTGTCTTTGGAGCGGCCGATGCGGTGATTAGTAGTTGGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 AGCAGGGGATCGAAAGACCTTGTCTTTGGAGCGGCCGATGCGGTGATTAGTAGTTGGT 242
Qy    241 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGAACCAGCCACAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGAACCAGCCACAC 302
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Db    181 AGCAGGGGATCGAAAGACCTTGTCTTTGGAGCGGCCGATGCGGTGATTAGTAGTTGGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC 300
Qy    301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 360
Qy    361 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCT 420
Qy    421 TTCAGTCGAGAGAGAAAAGGTTGTGACTAATAATCACAACTTATGATGTGTACCGACAGAAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTCAGTCGAGAGAGAAAAGGTTGTGACTAATAATCACAACTTATGATGTGTACCGACAGAAG 480
Qy    481 AAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCG 540
Qy    541 GAATTACTGGGCGTAAAGGGTGCGCAGGCGGTTGTAAGTCAGATGTGAAATCCCCGGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAATTACTGGGCGTAAAGGGTGCGCAGGCGGTTGTAAGTCAGATGTGAAATCCCCGGG 600
Qy    601 CTTAACCTGGGAATTGCTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTTAACCTGGGAATTGCTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAAT 660
Qy    661 TCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCCC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCCC 720
Qy    721 CCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACGATTAGATACCC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACGATTAGATACCC 780
Qy    781 TGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACG 840
Qy    841 TAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGA 900
Qy    901 ATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGTTTAATTCGATGCAACGCGAAAAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGTTTAATTCGATGCAACGCGAAAAA 960
Qy    961 CCTTACCTACCCTTGACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CCTTACCTACCCTTGACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACG 1020
Qy   1021 CTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC 1080
Qy   1081 GCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGCACTTTAATGAGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGCACTTTAATGAGACT 1140
Qy   1141 GCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTA 1200
Qy   1201 GGGCTTCACACGTGCTACAATGGCCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGGCTTCACACGTGCTACAATGGCCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTA 1260
Qy   1261 ATCTCAGAAAGGCGGTCGTAGTCCGGATCGGAGTCGGAGTCTCGCAACTCGACTCCGTGA 1320
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Qy   1380  CCGCCCGTCACACCATGGGAGTGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGG  1438
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1383  CCGCCCGTCACACCATGGGAGTGGTTTCACCAGAAGCAGATAGTCTAACCGTAAGGAGG  1442

Qy   1439  GCGTTTGCCACGGCGAGATTCATGACTGG  1467
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Db   1443  GCGTTTGCCACGGTGAGATTCATGACTGG  1471
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RESULT 3
CQ796927

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LOCUS       CQ796927             1491 bp    DNA     linear   PAT 19-APR-2004
DEFINITION  Sequence 20 from Patent WO2004026772.
ACCESSION   CQ796927
VERSION     CQ796927.1  GI:46408553
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Hovanec,T.A.
  TITLE     Ammonia-oxidizing bacteria and methods of using and detecting
            thesame
  JOURNAL   Patent: WO 2004026772-A 20 01-APR-2004;
            Aquaria Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1491
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="N. Aestuarii-like AOB BF16clone57 16S rDNA"
ORIGIN

Query Match       98.2%;   Score 1440.2;   DB 6;   Length 1491;
Best Local Similarity  99.7%;   Pred. No. 7.9e-18;
Matches 1464;   Conservative  0;   Mismatches  0;   Indels  3;   Gaps  2;
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Qy     1  TTGATCATGGCTCAGATTGAACCGTGGGCGCATGCTTTACACATGCAAGTCGAACGGCAG    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3  TTGATCATGGCTCAGATTGAACCGTGGGCGCATGCTTTACACATGCAAGTCGAACGGCAG    62

Qy    61  CACGGGTGCTTGCACCTGGTGCGACGGGTGAGTGGGTGAGTGAATGCATCGGACGTGTC   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    63  CACGGGTGCTTGCACCTGGTGCGACGGGTGAGTGGGTGAGTGAATGCATCGGACGTGTC   122

Qy   121  CAGAAGTGGGGATAACGATCGAAAGATGTCTAATAACGCCATATTCTTCTACGGAGGAA   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123  CAGAAGTGGGGATAACGATCGAAAGATGTCTAATAACGCCATATTCTTCTACGGAGGAA   182

Qy   181  AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGGCCGATGCCGATTAGCTAGTTGGT   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   183  AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGGCCGATGCCGATTAGCTAGTTGGT   242

Qy   241  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACAC   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243  GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACAC   302

Qy   301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG   362

Qy   361  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGAGG-CTTCGGGTTGTAAAGCTC   419
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   363  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGAGGCCTTCGGGTTGTAAAGCTC   422

Qy   420  TTTCAGTCGAGAAGAAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA   479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423  TTTCAGTCGAGAAGAAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA   482

Qy   480  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC   539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC   542

Qy   540  GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCGTTTGTAAGTCAGATGTGAAATCCCCGG   599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543  GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCGTTTGTAAGTCAGATGTGAAATCCCCGG   602

Qy   600  GCTTAACCTGGGAATTGCCTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGAA   659
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   603  GCTTAACCTGGGAATTGCCTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGAA   662

Qy   660  TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAGAACATCGATGGCGAAGGCAGCC   719
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   663  TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAGAACATCGATGGCGAAGGCAGCC   722

Qy   720  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC   779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   723  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC   782

Qy   780  CTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC   839
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Db   783  CTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC   842

Qy   840  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGG   899
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Db   843  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGG   902

Qy   900  AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTGCAACGCGAAAA   959
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Db   903  AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTGCAACGCGAAAA   962

Qy   960  ACCTTACCTACCCTTGACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC  1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   963  ACCTTACCTACCCTTGACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC  1022

Qy  1020  GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1023  GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1082

Qy  1080  CGCAACGAGCGCAACCCTTGTCATTTAGTTGCCATCAGTTCGGCTGGGCACTTTAATGAC  1139
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Db  1083  CGCAACGAGCGCAACCCTTGTCATTTAGTTGCCATCAGTTCGGCTGGGCACTTTAATGAC  1142

Qy  1140  TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGT  1199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1143  TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT  1202

Qy  1200  AGGGCTTCACACGTCATACAATGGCGCGTAATACAGAGGGTTGCCAACCCGCGAGGGGAGCT  1259
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1203  AGGGCTTCACACGTCATACAATGGCGCGTAATACAGAGGGTTGCCAACCCGCGAGGGGAGCT  1262

Qy  1260  AATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGG  1319
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1263  AATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGG  1322

Qy  1320  AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACA  1379
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1323  AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACA  1382
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ORGANISM    Nitrosomonas aestuarii
            Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
            Nitrosomonadaceae; Nitrosomonas.
REFERENCE   1 (bases 1 to 1450)
AUTHORS     Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
            Koops,H.P. and Wagner,M.
TITLE       Phylogeny of all recognized species of ammonia oxidizers based on
            comparative 16S rRNA and amoA sequence analysis: implications for
            molecular diversity surveys
JOURNAL     Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)
PUBMED      11097916
REFERENCE   2 (bases 1 to 1450)
AUTHORS     Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
            Koops,H.P. and Wagner,M.
TITLE       Direct Submission
JOURNAL     Submitted (26-MAY-2000) Lehrstuhl fuer Mikrobiologie, Technische
            Universitaet Muenchen, Am Hochanger 4, Freising 85350, Germany
FEATURES             Location/Qualifiers
     source          1..1450
                     /organism="Nitrosomonas aestuarii"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:52441"
     rRNA            <1..>1450
                     /product="16S ribosomal RNA"
ORIGIN

Query Match          96.9%;  Score 1421.2;  DB 1;  Length 1450;
Best Local Similarity 99.7%;  Pred. No. 1.7e-17;
Matches 1445;  Conservative    0;  Mismatches  3;  Indels  2;  Gaps  2;

Qy     17 TTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGAACGGCAGCGCAGGGTGCTTGCACC         76
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGAACGGCAGCGCAGGGTGCTTGCACC         60

Qy     77 TGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGGATAA        136
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Db     61 TGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGGATAA        120

Qy    137 CGCATCGAAAGATGTGCTAATACCGCATAATTCCTCTACGGGGAAGAAAGCAGGGGATCGAAAG        196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCATCGAAAGATGTGCTAATACCGCATAATTCCTCTACGGGGAAGAAAGCAGGGGATCGAAAG        180

Qy    197 ACCTTGTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTACC        256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ACCTTGTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTACC        240

Qy    257 AAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGG        316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGG        300

Qy    317 CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCC        376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCC        360

Qy    377 AGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTGAAAGCTCTTTCAGTCGAGAAGAA        435
          |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db    361 AGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTGAAAGCTCTTTCAGTCGAGAAGAA        420

Qy    436 AAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACGAGAAGAAGCACCGGCTAACT        495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAGGTTGTGACTAATAATCACAACTTATGACGGTACCGACGAGAAGAAGCACCGGCTAACT        480

Qy    496 ACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTA        555
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Db    481 ACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTA        540

Qy    556 AAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCGGGCTTAACCTGGGAATT        615
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCGGGCTTAACCTGGGAATT        600

Qy    616 GCGTTTGAAACTACAAAGCTAGAGTGTGAGAGGGGGTGAATTCCATGTGTAGCAGT        675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTTTGAAACTACAAAGCTAGAGTGTGAGAGGGGGTGAATTCCATGTGTAGCAGT        660

Qy    540 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCGG        599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCGG        602

Qy    600 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTGAGAGGGGGTGGAA        659
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTGAGAGGGGGTGGAA        662

Qy    660 TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC        719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    663 TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCC        722

Qy    720 CCCTGGGTTAACCACTGACGCTCATCATGACGAAAGCGTGGGGAGCAAACAGGATTAGATACC        779
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    723 CCCTGGGTTAACCACTGACGCTCATCATGACGAAAGCGTGGGGAGCAAACAGGATTAGATACC        782

Qy    780 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCCTTACTAGGCTTGGTAAC        839
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    783 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCCTTACTAGGCTTGGTAAC        842

Qy    840 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG        899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    843 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG        902

Qy    900 AATTGACGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA        959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    903 AATTGACGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA        962

Qy    960 ACCTTACCTACCCTTGACATGTAGCGGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC       1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    963 ACCTTACCTACCCTTGACATGTAGCGGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC       1022

Qy   1020 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC       1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1023 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC       1082

Qy   1080 CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTTAGTTGGGCACTTTAATGAGAC       1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1083 CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTTAGTTGGGCACTTTAATGAGAC       1142

Qy   1140 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT       1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1143 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT       1202

Qy   1200 AGGGCTTCACACGTCATACAATGGCGCGTACAGAGGGCTGCCAACCCGCGAGGGGGAGCT       1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1203 AGGGCTTCACACGTCATACAATGGCGCGTACAGAGGGCTGCCAACCCGCGAGGGGGAGCT       1262

Qy   1260 AATCTCAGAAAGCGCGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGG       1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1263 AATCTCAGAAAGCGCGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGG       1322

Qy   1320 AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACA       1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1323 AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACA       1382

Qy   1380 CCGCCCGTCACACCATGGGAGTGGGTTCACCAGAAGTAGTCTAACCGTAA-GAGG       1438
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1383 CCGCCCGTCACACCATGGGAGTGGGTTCACCAGAAGTAGTCTAACCGTAAGGAGG       1442

Qy   1439 GCGTTTGCCACGGGAGATTCATGACTGG       1467
          |||||||||||||||||||||||||||
Db   1443 GCGTTTGCCACGGGAGATTCATGACTGG       1471
```

RESULT 4
AF272420
LOCUS   AF272420   1450 bp   DNA   linear   BCT 05-DEC-2000
DEFINITION Nitrosomonas aestuarii 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF272420
VERSION   AF272420.1 GI:11545280
KEYWORDS   .
SOURCE   Nitrosomonas aestuarii

FEATURES   Location/Qualifiers
     source   1..1494
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="N. Aestuarii-like AOB P4clone31 16S rDNA"
ORIGIN

Query Match   95.7%;   Score 1403.4;   DB 6;   Length 1494;
Best Local Similarity   98.1%;   Pred. No. 3.4e-17;
Matches 1441;   Conservative   0;   Mismatches 26;   Indels 2;   Gaps 2;

Qy   1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG   63

Qy   61 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC 123

Qy   121 CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGGAGAA 180
           || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124 CGGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGGAGAA 183

Qy   181 AGCAGGGGATCGAAAGACCTTGTGCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT   240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 AGCAGGGGATCGAAAGACCTTGTGCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT   243

Qy   241 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC 303

Qy   301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   304 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAACG 363

Qy   361 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGTTGTAAAGCTC 419
           ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   364 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGTTGTAAAGCTC 423

Qy   420 TTTCAGTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   424 TTTCAGTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA 483

Qy   480 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   484 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 543

Qy   540 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCCCGG 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCCCGG 603

Qy   600 GCTTAACCTGGGAATTGCGTTTGAAACTGGCAAGCTAGAGTGTAGCAGAGGGGGGTGAA 659
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGAA 663

Qy   660 TTCCATGTGTAGCAGTGAAATGCGTAGAGATCGATGGCGAAGGCAGCGCC   719
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664 TTCCATGTGTAGCAGTGAAATGCGTAGAGATCGATGGCGAAGGCAGCGCC   723

Qy   720 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   724 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 783

Qy   780 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGGCCTTACTAGGCTTGGTAAC 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   784 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGGCCTTACTAGGCTTGGTAAC 843

Qy   840 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGG 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   844 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG 903

Qy   676 GAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCTGGGTTAACACTG 735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCTGGGTTAACACTG 720

Qy   736 ACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCC 795
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCC 780

Qy   796 TAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGTAGCTAACGCGGTGAA 855
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGTAGCTAACGCGGTGAA 840

Qy   856 GTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGAATTGACGGGGACCCG 915
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGAATTGACGGGGACCCG 900

Qy   916 CACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTG 975
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTG 960

Qy   976 ACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCTG 1035
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCTG 1020

Qy   1036 CATGGCTGTCGTCGTCTGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1095
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CATGGCTGTCGTCGTCTGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080

Qy   1096 CTTGTCATTAATTGCCATCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACCG 1155
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CTTGTCATTAATTGCCATCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACCG 1140

Qy   1156 GAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGTAGGGCTTCACACGTAA 1215
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGTAGGGCTTCACACGTAA 1200

Qy   1216 TACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGCG 1275
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGCG 1260

Qy   1276 TCGTAGTCCGGATCGCGGAATCGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCGC 1335
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TCGTAGTCCGGATCGCGGAATCGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCGC 1320

Qy   1336 GGATCACGATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCAT 1395
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGATCACGATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCAT 1380

Qy   1396 GGGAGTTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGGCGA 1454
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   1381 GGGAGTTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAAGGAGGGCGTTTGCCACGGTGA 1440

Qy   1455 GATTCATGAC 1464
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Db   1441 GATTCATGAC 1450

RESULT 5
CQ796926
LOCUS   CQ796926   1494 bp   DNA   linear   PAT 19-APR-2004
DEFINITION Sequence 19 from Patent WO2004026772.
ACCESSION   CQ796926
VERSION   CQ796926.1   GI:46408552
KEYWORDS   .
SOURCE   unidentified
  ORGANISM unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Hovanec.T.A.
  TITLE   Ammonia-oxidizing bacteria and methods of using and detecting
            thesame
  JOURNAL   Patent: WO 2004026772-A 19 01-APR-2004;

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ORIGIN

Query Match          94.6%;  Score 1388.2;  DB 1;  Length 1513;
Best Local Similarity 97.5%;  Pred. No. 6.1e-17;
Matches 1430;  Conservative  0;  Mismatches  34;  Indels  2;  Gaps  2;

Qy      1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG   60
            ||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||||
Db      6 TTGATTCTNGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG   65

Qy     61 CACGGGTGCTTGCACCTGGTGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 CACGGGTGCTTGCACCTGGTGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC  125

Qy    121 CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATAATGTCTTCTACGGAGGAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 CAGAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATAATGTCTTCTACGGAGGAAA  185

Qy    181 AGCAGGGGATCGAAAGACCTTGTCTTTGCTTGGACGGCCGATGCCTGATTAGCTAGTTGGT  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 AGCAGGGGATCGTAAGACCTTGCGCCTTGGACGGCCGATGCCTGATTAGCTAGTTGGT  245

Qy    241 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTGGTCTGAGAGGACGACCAGCCACAC  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 GGGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTGGTCTGAGAGGACGACCAGCCACAC  305

Qy    301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  365

Qy    361 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAG-CTTCGGGTTGTAAAGCTC  419
            ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    366 GGCGCAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTC  425

Qy    420 TTTCAGTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGTACCGACAGAA  479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 TTTCAGTCGAGAAGAAAGATTGTGATGAATAATCGCAATTCATCATGACGTATCGACAGAA  485

Qy    480 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  539
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  545

Qy    540 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGTTTGTAAGTCAGATGTGAAATCCCCGG  599
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 GGAATTACTGGGCGTAAAGGGTGCGCAGGCGGTTTGTAAGTCAGATGTGAAATCCCCGG  605

Qy    600 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA  659
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAACAGAGGGGGGTGGAA  665

Qy    660 TTCCATGTGTAGCAGTGAAATGCGTAGAGATCATGAGGAACACCGGTGGCGAAGGCAGCC  719
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 TTCCATGTGTAGCAGTGAAATGCGTAGAGATCATGAGGAACACCGGTGGCGAAGGCAGCT  725

Qy    720 CCCTGGGTTAACACTGACGCTCATGCAGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC  779
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 CCCTGGGTTAACACTGACGCTCATGCAGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC  785

Qy    780 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC  839
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTAGTAAC  845

Qy    840 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  899
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  905

Qy    900 AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  959
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  965

Qy    960 ACCTTACCTACCCTTGACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAAC 1019
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 ACCTTACCTACCCTTGACATGTAGCGAATATTTTCTAGAGATAGTAGTGCCTTCGGGAAC 1025

Qy    900 AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  959
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  963

Qy    960 ACCTTACCTACCCTTGACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAAC 1019
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 ACCTTACCTACCCTTGACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAAC 1023

Qy   1020 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1079
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1083

Qy   1080 CGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTTAGTTGGGCACTTTAATGAGAC 1139
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 CGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTTAGTTGGGCACTTTAATGAGAC 1143

Qy   1140 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT 1199
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT 1203

Qy   1200 AGGGCTTCACACGTAATACAATGGCCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1259
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 AGGGCTTCACACGTAATACAATGGCCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1263

Qy   1260 AATCTCAGAAAGCCGGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTCCGTGAAGTCGG 1319
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 AATCTCAGAAAGCCGGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTCCGTGAAGTCGG 1323

Qy   1320 AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1379
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1383

Qy   1380 CCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGCAGATAGTCTAACCGT-AAGAGG 1438
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   1384 CCGCCCGTCACACCATGGGAGTTGGCTGCACCAGAAGTAGTGCTTGCTAACCCTCGGGGAGG 1443

Qy   1439 GCGTTTGCCACGGCGAGATTCATGACTGG 1467
            |||||||||| |||||
Db   1444 ACGCTTACCACGGTGTGTGCAATGACTTG 1472
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RESULT 6
AF272424
LOCUS   AF272424   1513 bp   DNA   linear   BCT 05-DEC-2000
DEFINITION Nitrosomonas sp. NM 51 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF272424
VERSION   AF272424.1 GI:11545284
KEYWORDS   .
SOURCE   Nitrosomonas sp. Nm51
  ORGANISM Nitrosomonas sp. Nm51
            Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
            Nitrosomonadaceae; Nitrosomonas.
REFERENCE   1 (bases 1 to 1513)
  AUTHORS   Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
            Koops,H.P. and Wagner,M.
  TITLE   Phylogeny of all recognized species of ammonia oxidizers based on
            comparative 16S rRNA and amoA sequence analysis: implications for
            molecular diversity surveys
  JOURNAL   Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)
   PUBMED   11097916
REFERENCE   2 (bases 1 to 1513)
  AUTHORS   Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
            Koops,H.P. and Wagner,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (26-MAY-2000) Lehrstuhl fuer Mikrobiologie, Technische
            Universitaet Muenchen, Am Hochanger 4, Freising 85350, Germany
FEATURES   Location/Qualifiers
     source   1..1513
                     /organism="Nitrosomonas sp. Nm51"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:133720"
     rRNA   <1..>1513
                     /product="16S ribosomal RNA"

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Qy          1 ACGGCTGGGCGCATGCTTTACACATGCAAGTCGAACGGCAGCGGACGCACGGGTGCTTGCACCTGGT 60
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Db         81 GGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTCCAGAGAGTGGGGGATAACGCA 140
              ||||||||||||||| |||||||||||||||||||||||||||||||||
Db         61 GGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTCCAAGAGTGGGGGATAACGCA 120

Qy        141 TCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAAGACCT 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCGAAAGATGTGCTAATACCGCATATTCTCTAAGGAGGAAAAGCAGGGGATCGTAAGACCT 180

Db        201 TGTGCTTTGGAGCGGCCGATGCGTGATTAGCTAGTTGGTGGTGGTAAAGGCCTACCAAGG 260
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Qy        181 TGCCCTTTTGGAGTGGCCGATGCGTGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAGG 240

Qy        261 CAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGCCCA 320
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Db        241 CGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAAGACACGGCCCA 300

Db        321 GACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCA 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        301 GACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCA 360

Qy        381 ATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAAGAAGAAAGG 439
              ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        361 ATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGAAGAAGAAAGA 420

Db        440 TTGTGACTAATAATCACAACTTATGTGTACGGACAGAAGAAGCACCGGCTAACTACGT 499
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        421 TTGTGATGAATAATCACAATTCATGAGTATCGACGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGG 480

Db        500 GCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGG 559
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Qy        481 GCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGG 540

Qy        560 GTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAATTGCGT 619
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Db        541 GTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAATTGCGT 600

Qy        620 TTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAGTGAAA 679
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Db        601 TTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAGTGAAA 660

Qy        680 TGGGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCTGGGGTAACACTGACGC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCTGGGGTAACACTGACGC 720

Db        740 TCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAA 799
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Qy        721 TCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAA 780

Qy        800 CGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTGTAACGGCGTGAAGTTG 859
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Db        781 CGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTGTAACGGCGTGAAGTTG 840

Db        860 ACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCCGCACA 919
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Qy        841 ACCGCCTGGGGAGTACGGTCGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCCGCACA 900

Qy        920 AGCGGTGGATTAATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACAT 979
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Db        901 AGCGGTGGATTAATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACAT 960

Qy        980 GTAGGGAATATTTGAGATAAATAGTGCCTTCGGGAACGCTAACACAGTGCTGCATG 1039
              ||| ||||||||||| ||||||||| || || |||||||||||||||||||||||||||
Db        961 GTAGCGAATTTCTAGAGATAGATTAGTGCCTTCGGGAACGCTAACACAGTGCTGCATG 1020

Qy       1040 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACCCTTG 1099
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Db       1021 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACCCTTG 1080

Qy       1100 TCATTAATTGCCATCATTAGTTGGGCACTTAATGAGACTGCCGGTGACAAACCGGAGG 1159
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Qy       1020 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1079
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Db       1026 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1085

Qy       1080 CGCAACGAGCGCAACCCTTGTCATTCATTAATTGCCATCATTTAGTTGGGCACTTAATGAGAC 1139
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Db       1086 CGCAACGAGCGCAACCCTTGTCATTCATTAATTGCCATCATTTAGTTGGGCACTTAATGAGAC 1145

Db       1140 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT 1199
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       1146 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT 1205

Db       1200 AGGGCTTCACACGTCATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1259
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       1206 AGGGCTTCACACGTCATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT 1265

Db       1260 AATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGG 1319
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       1266 AATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGG 1325

Qy       1320 AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1379
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Db       1326 AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1385

Qy       1380 CCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGTAGTCTAACCGTAA-GAGG 1438
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1386 CCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGTAGTCTAACCGCAAGGAGG 1445

Db       1439 GCGTTTGCCACGGCGAGATTCATGAC 1464
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Db       1446 GCGTTTGCCACGGTGAGATTCATGAC 1471
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RESULT 7
AF272418
LOCUS   AF272418   1492 bp   DNA   linear   BCT 05-DEC-2000
DEFINITION Nitrosomonas marina 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF272418
VERSION   AF272418.1 GI:11545278
KEYWORDS   .
SOURCE   Nitrosomonas marina
  ORGANISM Nitrosomonas marina
            Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
            Nitrosomonadaceae; Nitrosomonas.
REFERENCE   1 (bases 1 to 1492)
  AUTHORS   Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
            Koops,H.P. and Wagner,M.
  TITLE   Phylogeny of all recognized species of ammonia oxidizers based on
            comparative 16S rRNA and amoA sequence analysis: implications for
            molecular diversity surveys
  JOURNAL   Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)
   PUBMED   11097916
REFERENCE   2 (bases 1 to 1492)
  AUTHORS   Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
            Koops,H.P. and Wagner,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (26-MAY-2000) Lehrstuhl fuer Mikrobiologie, Technische
            Universitaet Muenchen, Am Hochanger 4, Freising 85350, Germany
FEATURES   Location/Qualifiers
     source   1..1492
                     /organism="Nitrosomonas marina"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:917"
     rRNA   <1..>1492
                     /product="16S ribosomal RNA"
ORIGIN

Query Match   93.9%; Score 1377; DB 1; Length 1492;
Best Local Similarity 97.8%; Pred. No. 9.6e-17;
Matches 1417; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

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Qy         21 ACGGCTGGGCGCATGCTTTACACATGCAAGTCGAACGGCAGCGGACGCACGGGTGCTTGCACCTGGT 80
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Qy    136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 195
          |||||||||||||||||||||||||||||| ||||| |||||||||||||||||||||||
Db    121 ACGCATCGAAAGATGTGCTAATACCGCATATCTCTAAGGAGGAAAGCAGGGGATCGAAA 180

Qy    196 GACCTTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
          ||||||| |||||||||||||||||| |||||||||||||||||||||||||||||||
Db    181 GACCTTGCGCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 240

Qy    256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 315
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 300

Qy    316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
          |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db    301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCAAGCCTGATC 360

Qy    376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCCGGTTGTAAAGCTCTTTCAGTCGAGAAGA 434
          ||||||||||||||||||||||||||  ||| |||||||||||||||||||||||||||
Db    361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 420

Qy    435 AAAGGTTGTGACTAATAATCACAACTTATGATGTGACAGAGAAGCACCGGCTAAC 494
          |||||||  |  ||||||||| ||    ||| | |||||||||||||||||||||
Db    421 AAAGGTTACGGTAAAATAATCGTGACTCATCATGACGTGACAGAGAAGAAGCACCGGCTAAC 480

Qy    495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 540

Qy    555 AAAGGGTGCGCAGGCGGCGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 614
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAAGGGTGCGCAGGCGGCGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 600

Qy    615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 674
          |||||||||||||||||  ||||||||| ||||||||||||||||||||||||||||||
Db    601 TGCGTTTGAAACTACAAGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 660

Qy    675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACT 734
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Db    661 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCTCTGGGTTAACACT 720

Qy    735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGTCCACGCC 794
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Db    721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGTCCACGCC 780

Qy    795 CTAAACGATGTCAACTAGTTGTTGGGGCTTACTAGGGCTTGGTAACGTAGCTAACGCGTGA 854
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Db    781 CTAAACGATGTCAACTAGTTGTTGGGGCTTATTAGGCTTGGTAACGTAGCTAACGCGTGA 840

Qy    855 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 914
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Db    841 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 900

Qy    915 GCACAAGCGGTGGAGTGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 974
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 960

Qy    975 GACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
          ||||||||||||||  | ||||||||  || ||||| |||||||||||||||||||||||
Db    961 GACATGTAGCGAATTTTCTAGAGATAGATAGTAGTGC-TTCGGGAACGCTAACACAGGTGCT 1019

Qy   1035 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1079

Qy   1095 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1154
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   1080 CCTTGTCATTAATTGCCATCATTTGGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1139

Qy   1155 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACGTA 1214
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACGTA 1199

Db   1081 TCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACCGGAGG 1140

Qy   1160 AAGGTGGGGATGACGTCAAGTCCTCAGGGCCTTATGGGTAGGGCTTCACACGTAATACA 1219
          |||||||||||||||||||||||    |||||||||||||||||||||||||||||||
Db   1141 AAGGTGGGGATGACGTCAAGTCAAGTCCCTTATGGGTAGGGCTTCACACGTAATACA 1200

Qy   1220 ATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGCGCGTCGT 1279
          |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db   1201 ATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTAATCCCAGAAAGCGCGTCGT 1260

Qy   1280 AGTCCGGATCGGAGTCTGCACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCGCGGAT 1339
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Db   1261 AGTCCGGATCGGAGTCTGCGACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCGCGGAT 1320

Qy   1340 CAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACATGGGA 1399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGA 1380

Qy   1400 GTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGGCGAGATT 1458
          |||||||||||||||||||||||||||||||  || |||||||||||||||||| ||||
Db   1381 GTGGGTTTCACCAGAAGCAGATAGTCTAACCCAAGGAGGGCGTTTGCCACGGCGGTGAGATT 1440

Qy   1459 CATGACTGG 1467
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Db   1441 CATGACTGG 1449
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RESULT 8

AF386752

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LOCUS       AF386752               1457 bp    DNA     linear   ENV 10-MAY-2004
DEFINITION  Nitrosomonas sp. R7c131 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF386752
VERSION     AF386752.1  GI:17864829
KEYWORDS    ENV.
SOURCE      Nitrosomonas sp. R7c131
  ORGANISM  Nitrosomonas sp. R7c131
            Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
            Nitrosomonadaceae; Nitrosomonas; environmental samples.
REFERENCE   1  (bases 1 to 1457)
  AUTHORS   Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
  TITLE     Identification of bacteria responsible for ammonia oxidation in
            freshwater aquaria
  JOURNAL   Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
   PUBMED   11722936
REFERENCE   2  (bases 1 to 1457)
  AUTHORS   Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria
            Group, 6100 Condor Dr, Moorpark, CA 93021, USA
FEATURES             Location/Qualifiers
     source          1..1457
                     /organism="Nitrosomonas sp. R7c131"
                     /mol_type="genomic DNA"
                     /isolation_source="ammonia-oxidizing bacteria isolated
                     from freshwater aquaria enrichments"
                     /db_xref="taxon:180511"
                     /clone="R7c131"
                     /environmental_sample
     rRNA            <1..>1457
                     /product="16S ribosomal RNA"
ORIGIN
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Query Match      92.7%;  Score 1360.4;  DB 3;  Length 1457;
Best Local Similarity   97.3%;  Pred. No. 1.9e-16;
Matches 1415;  Conservative   0;  Mismatches 36;  Indels  3;  Gaps  3;

Qy     16 ATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGCTTGCAC 75
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Db      1 ATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGCGATGCTTGCAT 60

Qy     76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA 135
          ||||||||||||||||||||||||||||||||||||||||||  ||||||| ||||||||
Db     61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTCCTCAGAAGAGAGGGGGTA 120
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Qy   1215 ATACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 ATACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1259

Qy   1275 GTCGTAGTCCGATCGGAGTCTTGCAACTCGACTCCGTGAAGTCGGAATCGTCTAGTAATCG 1334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 GTCGTAGTCCGATCGGAGTCTCGCAACTCGACTCCGTGAAGTCGGAATCGTCTAGTAATCG 1319

Qy   1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1379

Qy   1395 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGGCG 1453
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   1380 TGGGAGTGGGTTTCACCAGAAGCAGTAGTCTAACCGTAAGGAGGGCGTTTGCCACGGTG 1439

Qy   1454 AGATTCATGACTGG 1467
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Db   1440 AGATTCATGACTGG 1453
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RESULT 9
AF386753
LOCUS       AF386753                 1457 bp    DNA     linear   ENV 10-MAY-2004
DEFINITION  Nitrosomonas sp. R7c140 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF386753
VERSION     AF386753.1  GI:17864830
KEYWORDS    ENV.
SOURCE      Nitrosomonas sp. R7c140
  ORGANISM  Nitrosomonas sp. R7c140
            Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
            Nitrosomonadaceae; Nitrosomonas; environmental samples.
REFERENCE   1  (bases 1 to 1457)
  AUTHORS   Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
  TITLE     Identification of bacteria responsible for ammonia oxidation in
            freshwater aquaria
  JOURNAL   Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
   PUBMED   11722936
REFERENCE   2  (bases 1 to 1457)
  AUTHORS   Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria
            Group, 6100 Condor Dr, Moorpark, CA 93021, USA
FEATURES             Location/Qualifiers
     source          1..1457
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                     /mol_type="genomic DNA"
                     /isolation_source="ammonia-oxidizing bacteria isolated
                     from freshwater aquaria enrichments"
                     /db_xref="taxon:180543"
                     /clone="R7c140"
                     /environmental_sample
     rRNA            <1..>1457
                     /product="16S ribosomal RNA"
ORIGIN
Query Match     92.6%;  Score 1358.8;  DB 3;  Length 1457;
Best Local Similarity   97.2%;  Pred. No. 2e-16;
Matches 1414;  Conservative    0;  Mismatches  37;  Indels   3;  Gaps    3;
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Qy     16 ATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGCGACACGGGTGCTTGCAC 75
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Db      1 ATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGCGACACGGGTGCTTGCAT 60

Qy     76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA 135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTATCCAGAAGAGGGGGGTA 120

Qy    136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 195
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Db    121 ACGCATCGAAAGATGTCTAATACCGCATATATCCTCTAAGGAGGAAAGCAGGGGACTCGAAA 180

Qy    196 GACCTTCGTGCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
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Db    181 GACCTTCGTGCTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 240

Qy    256 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 300

Qy    316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
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Db    301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC 360

Qy    376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGTTGTAAAGCTCTTTCAGTCGAGAGA 434
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Db    361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAGA 420

Qy    435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC 494
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Db    421 AAAGGTTACGTTAAATAATCGTGACTCATGACGGTATCGGACGAAGAAGCACCGGCTAAC 480

Qy    495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554
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Db    481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 540

Qy    555 AAAGGGTGCGCAGGCGGCTTGGTAAGTCAGATGTGAAATCCCGGGGCTTAACCTGGGAAT 614
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Db    541 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCGGGGCTTAACCTGGGAAT 600

Qy    615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 674
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Db    601 TGCGTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 660

Qy    675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCTGGGTAACACT 734
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Db    661 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCTCCTGGGTAACACT 720

Qy    735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 794
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Db    721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 780

Qy    795 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAGTAGTCAACGCGTGA 854
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Db    781 CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCTTGGTAGTAGTCAACGCGTGA 840

Qy    855 AGTTGACGCGCTCGGGGAGTACCGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 914
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Db    841 AGTTGACGCGCTCGGGGAGTACCGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 900

Qy    915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 974
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Db    901 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 960

Qy    975 GACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
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Db    961 GACATGTAGCGAATTTCTAGAGATAGTAGTGC-TTCGGCAACGCTAACACAGGTGCT 1019

Qy   1035 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
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Db   1020 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1079

Qy   1095 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1154
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Db   1080 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1139

Qy   1155 GGAGGAAGGTGGGGATGACGTCAAGTCCTCAAGTCCCTTATGGGCCTTATGGGGGATA 1214
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Db   1140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCAAGTCCCTTATGGGCCTTATGGGGGGGTA 1199

Qy   1215 ATACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGGC 1274
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Db   1200 ATACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGGC 1259

Qy   1275 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG 1334
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Db   1260 GTCGTAGTCCGGATCGGAGTCTCGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG 1319
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Db   1260 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG 1319
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Db   421 AAAGGTTACGGTAAATAATCGTGACTCATGACGTATCGACAGAAGAAGCACCGGCTAAC 480

Qy   1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
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Qy   495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554

Db   1320 CGGATCAGCAGCGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1379
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Db   481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 540

Qy   1395 TGGGAGTGGGTTTCACCAGAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGGCG 1453
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Qy   555 AAAGGGTGCGCAGGCGGCTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 614

Db   1380 TGGGAGTGGGTTTCACCAGAGCAGATAGTCTAACCGTAGGAGGGGCGCTTGCCACGGCG 1439
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Db   601 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 600

Qy   1454 AGATTCATGACTGG 1467
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Qy   615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 674

Db   1440 AGATTCATGACTGG 1453

Db   661 TGCGTTTGAAACTACAAGGCTAGAGTGTGCAGAGGGTGGAATTCCATGTGTAGCAG 660

RESULT 10
CQ796908
LOCUS   CQ796908   1457 bp   DNA   linear   PAT 19-APR-2004
DEFINITION Sequence 1 from Patent WO2004026772.
ACCESSION   CQ796908
VERSION   CQ796908.1   GI:46408534
KEYWORDS   .
SOURCE   unidentified
  ORGANISM unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Hovanec,T.A.
  TITLE   Ammonia-oxidizing bacteria and methods of using and detecting
            the same
  JOURNAL   Patent: WO 2004026772-A 1 01-APR-2004;
            Aquaria Inc. (US)
FEATURES   Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
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ORIGIN

Query Match   92.6%;   Score 1358.8; DB 6; Length 1457;
Best Local Similarity 97.2%;   Pred. No. 2e-16;
Matches 1414; Conservative   0;   Mismatches   37; Indels   3; Gaps   3;

Qy   16 ATTGAACGCTGGCGGCCATGTCTTTACACATGCAAGTCGAACGGCAGCACGGGGTGCTTGCAC 75
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Db   1 ATTGAACGCTGGCGGCCATGTCTTTACACATGCAAGTCGAACGGCAGCACGATGCTTGCAT 60

Qy   76 CTGTGTGGCGAGTGGCGGACGGGTGAGTAATACGCATATTCTACGGAAGTGTCCAGAAGTGGGGGATA 135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTGTGTGGCGAGTGGCGGACGGGTGAGTAATGCGCATATTCTACGGAAGTGTCCAGAAGGGGGGGTA 120

Qy   136 ACGGATCGAAAGATGTGCTAATACCGCATATTCTCACGGAGGAAAGAGGGGATCGAAA 195
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Db   121 ACGGATCGAAAGATGTGCTAATACCGCATATACTTCTAAGGAGGAAAGCAGGGGATCGAAA 180

Qy   196 GACCTTGTGCTTTTGGAGCGGCGCCGATGGCCCGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GACCTTGTGGCCTTTTGGAGCGGCGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 240

Qy   256 CAAGGCAACAACGATCAGTAGTTGGTCGGAGACGATCGGCCACCAGCCACACTGGGACTGAGACACG 315
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Db   241 CAAGGCGACGATCAGTAGTTGGTCGGAGACGATCGGCCACCAGCCACACTGGGACTGAGACACG 300

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
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Db   301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC 360

Qy   376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 434
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 420

Qy   435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC 494
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RESULT 11
CS089154

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LOCUS           CS089154                1457 bp    DNA     linear   PAT 25-MAY-2005
DEFINITION      Sequence 1 from Patent EP1502948.
ACCESSION       CS089154
VERSION         CS089154.1  GI:66714438
KEYWORDS        .
SOURCE          unidentified
  ORGANISM      unidentified
                unclassified.
REFERENCE       1
  AUTHORS       Hovanec,T.A. and Burrel,P.C.
  TITLE         Ammonia-oxidizing bacteria
  JOURNAL       Patent: EP 1502948-A 1 02-FEB-2005;
                Aquaria Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
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                     ammonia-oxidizing bacterium represented by R7 clone140"
ORIGIN

Query Match         92.6%;  Score 1358.8;  DB 6;  Length 1457;
Best Local Similarity   97.2%;  Pred. No. 2e-16;
Matches 1414;  Conservative    0;  Mismatches   37;  Indels    3;  Gaps    3;

Qy     16 ATTGAACGCTGGCGCATGCTTACACATGCAAGTCGAACGGCAGCAGCACGGGTGCTTGCAC   75
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Db      1 ATTGAACGCTGGCGCATGCTTACACATGCAAGTCGAACGGCAGCAGCACGATGCTTGCAT   60

Qy     76 CTGGTGGGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA  135
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Db     61 CTGGTGGGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGAGAGGGGTA  120

Qy    136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA  195
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Db    121 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTAAGGAGGAAAGCAGGGGATCGAAA  180

Qy    196 GACCTTGCGTTTTGGAGCGGCCGCATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC  255
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Db    181 GACCTTGCGCTTTGAGCGGCCGCATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC  240

Qy    256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  315
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Db    241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  300

Qy    316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAAGCCTGATC  375
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Db    301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC  360

Qy    376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTGAAAGCTCTTTCAGTCGAGAGA  434
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Db    361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTGAAAGCTCTTTCAGTCGAGAGA  420

Qy    435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC  494
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Db    421 AAAGGTTACGGTAAATAATCGTCGACTCATGACGGTACCGTAATCGGAAGGCACCGGCGT  480

Qy    495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  540

Qy    555 AAAGGGTGCGCAGGCGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT  614
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Db    541 AAAGGGTGCGCAGGCGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT  600

Qy    615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGAATTCCATGTGTAGCAG  674
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Db    601 TGCGTTTGAAACTACAAGCTAGAGTGTGGCAGAGGGGGGTGAATTCCATGTGTAGCAG  660

Qy    675 TGAAATGCGTAGAGATGGAAGGAACACCGATGGCGAAGGCAGCCCCCTGGGTTAACACT  734
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Db    661 TGAAATGCGTAGAGATGGAAGGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACT  720

Qy    735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  794
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Db    721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  780

Qy    795 CTAAACGATGTCAACTAGTTGTTGGGCTTACTAGGCCTTACTAGTAGTAACGCGTAA  854
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Db    781 CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCCTTAGGCTGTAACGAGCTAACGCGTGA  840

Qy    855 AGTTGACCCGCCTGGGGAGTACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGACCC  914
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Db    841 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC  900

Qy    915 GCACAAGCGGTGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  974
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Db    901 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  960

Qy    975 GACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT  1034
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Db    961 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC-TTCGGGAACGCTAACACAGGTGCT  1019

Qy   1035 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC  1094
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Db   1020 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC  1079

Qy   1095 CCTTGTCATTAATTGCCATCATCATTAGTTGGGACTCTTAATGAGACTGCCGGTGACAAACC  1154
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Db   1080 CCTTGTCATTAATTGCCATCATCATTTGGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC  1139

Qy   1155 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGCTAGGCTTCACACGTA  1214
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Db   1140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA  1199

Qy   1215 ATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC  1274
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Db   1200 ATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC  1259

Qy   1275 GTCGTAGTCCGGATCGCGAGTCTGCAACTCGACTCCGTGAAGTCGAATCGCTAGTAATCG  1334
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Db   1260 GTCGTAGTCCGGATCGCGAGTCTGCAACTCGACTCCGTGAAGTCGAATCGCTAGTAATCG  1319

Qy   1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA  1394
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Qy   1395 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGGCG  1453
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Db   1380 TGGGAGTGGGTTTCACCAGAAGCAGGTAGTCTAACCGTAAGGAGGGCGCTTGCCACGGTG  1439

Qy   1454 AGATTCATGACTGG  1467
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Db   1440 AGATTCATGACTGG  1453
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RESULT 12
CS089155
LOCUS           CS089155                1457 bp    DNA     linear   PAT 25-MAY-2005
DEFINITION      Sequence 2 from Patent EP1502948.
ACCESSION       CS089155
VERSION         CS089155.1  GI:66714439
KEYWORDS        .
SOURCE          unidentified
  ORGANISM      unidentified
                unclassified.
REFERENCE       1
  AUTHORS       Hovanec,T.A. and Burrel,P.C.
  TITLE         Ammonia-oxidizing bacteria
  JOURNAL       Patent: EP 1502948-A 2 02-FEB-2005;
                Aquaria Inc. (US)
FEATURES             Location/Qualifiers
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        /db_xref="taxon:32644"
        /note="Description of Unknown Organism: AOB Type A1
        ammonia-oxidizing bacterium represented by R7 clone187"

ORIGIN

Query Match        92.6%;  Score 1358.8;  DB 6;  Length 1457;
Best Local Similarity  97.2%;  Pred. No. 2e-16;
Matches 1414;   Conservative   0;  Mismatches  37;  Indels   3;  Gaps   3;

Qy    16 ATTGAACGCTGGCGCGCATGCTTTACACATGCGAACGCGCAGCACGCGGTGCTTGCAC 75
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db     1 ATTGAACGCTGGCGCGCATGCTTTACACATGCGAACGCGCAGCACGCGGTGCTTGCAT 60

Qy    76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAAGAGTGGGGGATA 135
            |||||||||||||||||||||||||||||||||| ||||||||||||||
Db    61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAAGAGAGGGGGGTA 120

Qy   136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 195
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTAAGGAGGAAAGCAGGGGATCGAAA 180

Qy   196 GACCTTGTGCTTTTGGAGCGGCCGATGCGTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GACCTTGCGCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 240

Qy   256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 315
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 300

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
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Db   301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC 360

Qy   376 CAGCAATGCCGCGTGAGTGAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 434
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Db   361 CAGCAATGCCGCGTGAGTGAGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 420

Qy   435 AAAGGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGCACCGGCTAAC 494
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Db   421 AAAGGGTTACGGTAAAATATCGTGACTCATGACGGTATCGACAGAAGAAGCACCGGCTAAC 480

Qy   495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554
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Db   481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 540

Qy   555 AAAGGGTGCGCAGGCGGCGGCGTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 614
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGGGTGCGCAGGCGGCGGCGTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 600

Qy   615 TGCGTTTGAAACTACAAAGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 674
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Db   601 TGCGTTTGAAACTACAAAGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 660

Qy   675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACT 734
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Db   661 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCTCTGGGTTAACACT 720

Qy   735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 794
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Db   721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 780

Qy   795 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGTAACGCGTGA 854
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Db   781 CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCTTGGTAACGCAGCTAACGCGTGA 840

Qy   855 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 914
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Db   841 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 900

Qy   915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 974
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Db   901 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 960

Qy   975 GACATGTAGCGAATATTTTAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   961 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC-TTCGGGAACGCTAACACAGGTGCT 1019

Qy  1035 GCATGGCTGCGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCGCAACGAGCGCAAC 1094
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Db  1020 GCATGGCTGCGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCGCAACGAGCGCAAC 1079

Qy  1095 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTAATGAGACTGCCGGTGACAAACC 1154
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1080 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTAATGAGACTGCCGGTGACAAACC 1139

Qy  1155 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1214
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Db  1140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1199

Qy  1215 ATACAATGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1274
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Db  1200 ATACAATGGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1259

Qy  1275 GTCGTAGTCCGGATCGGAGTCTGCAACTGCACTCCGTGAAGTCGAATCGCTAGTAATCG 1334
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1260 GTCGTAGTCCGGATCGGAGTCTGCAACTGCACTCCGTGAAGTCGAATCGCTAGTAATCG 1319

Qy  1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
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Db  1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1379

Qy  1395 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTGCCACGGCG 1453
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  1380 TGGGAGTGGGTTTCACCAGAAGCAGTAGTCTAACCGTAAGTCTAACCGTAAGGAGGGCGCTTGCCACGGTG 1439

Qy  1454 AGATTCATGACTGG 1467
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Db  1440 AGATTCATGACTGG 1453


RESULT 13
AX316092
LOCUS       AX316092     1457 bp    DNA      linear      PAT 14-DEC-2001
DEFINITION  Sequence 1 from Patent WO0190312.
ACCESSION   AX316092
VERSION     AX316092.1   GI:17899283
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Hovanec,T.A. and Burrell,P.C.
  TITLE     Ammonia-oxidizing bacteria
  JOURNAL   Patent: WO 0190312-A 1 29-NOV-2001;
            AQUARIA, INC. (US)
FEATURES             Location/Qualifiers
     source          1..1457
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="AOB Type A ammonia-oxidizing bacterium represented
                     by R7 clone140"

ORIGIN

Query Match        92.6%;  Score 1358.8;  DB 6;  Length 1457;
Best Local Similarity  97.2%;  Pred. No. 2e-16;
Matches 1414;   Conservative   0;  Mismatches  37;  Indels   3;  Gaps   3;

Qy    16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCGGCACGCGGTGCTTGCAC 75
            |||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db     1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCGGATGCAT 60

Qy    76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGCCCAGAAGTGGGGGATA 135
            ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTATCCGAAGAGGGGGGTA 120
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Qy    136  ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGCGAGGGAAGCAGGGGATCGAAA  195
           ||||||||||||||||||||||||||||| |||||  |||||||||||||||||||||||
Db    121  ACGCATCGAAAGATGTGCTAATACCGCATATACTCTAAGGACGAAAGCAGGGGATCGAAA  180

Qy    196  GACCTTGTGCTTTGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC  255
           ||||||| |||| |||||||||||||| ||||||||||||||||||||||||||||||
Db    181  GACCTTGCGCTTTGGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC  240

Qy    256  CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  300

Qy    316  GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC  375
           |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    301  GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC  360

Qy    376  CAGCAATGCCGCGTGAGTGAGGAAG-CTTCGGGTTGTGAAAGCTCTTTCAGTCGAGAGA  434
           ||||||| ||||| |||||||||||  |||||| |||||||||||||||| ||||||||
Db    361  CAGCAATGCCGCGTGAGTGAGGAAGGCCTTCGGGTTGTGAAAGCTCTTTCAGTCGAGAGA  420

Qy    435  AAAGGTTGTGACTAATAATCACAACTTATGATGATGGTACCGACGAAGAAGCACCGGCTAAC  494
           ||| ||    |||    || | |  || ||||||||||||||||||||||||||||||||
Db    421  AAAGGTTACGGTAAATAATCGTGACTCATGACCGGTATCGACGGTATCGGAATTACTGGGCGT  480

Qy    495  TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  540

Qy    555  AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT  614
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT  600

Qy    615  TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG  674
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Db    601  TGCGTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCATGTGTAGCAG  660

Qy    675  TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACT  734
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    661  TGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACT  720

Qy    735  GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  780

Qy    795  CTAAACGATGTCAACTAGTTGTTGGGCCTTGGGCTTGGTAAGTCAACGCTAGCGTTGA  854
           |||||||||||||||||||||||| |||||||||||| ||||||||||||||||| ||
Db    781  CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCTTGGTAACGCTAGCGTTGAGCGTGA  840

Qy    855  AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC  914
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Db    841  AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC  900

Qy    915  GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  974
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Db    901  GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  960

Qy    975  GACATGTAGCGGAATATTTTAGAGATAAAAATAGTGCCTTCGGGAACCGCTAACACAGTGCT  1034
           |||||||||||||||||||| ||||||| |||||||| ||||||||||||||||||||||
Db    961  GACATGTAGCGGAATTTTCTAGAGATAGATAGTGCC-TTCGGGAACCGCTAACACAGTGCT  1019

Qy   1035  GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC  1094
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Db   1020  GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC  1079

Qy   1095  CCTTGTCATTAATTGCCATCATTTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC  1154
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Db   1080  CCTTGTCATTAATTGCCATCATTTGGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC  1139

Qy   1155  GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGGCTTCACACGTA  1214
           ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   1140  GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGGCTTCACACGTA  1199

Qy   1215  ATACACAATGGCGCGTACAGAGGGCTGCCAACCCGCGAGGGGGAGCTAATCTCAAAAAGCGC  1274
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Db   1200  ATACACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC  1259

Qy   1275  GTCGTAGTCCGGATCGCAGTCGGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG  1334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260  GTCGTAGTCCGGATCGCAGTCGGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG  1319

Qy   1335  CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA  1394
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Db   1320  CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA  1379

Qy   1395  TGGGAGTGGGTTTCACCAGAAGCAGCAGTAGTCTAACCGTAA-GAGGGCGCTTGCCACGCG  1453
           ||||||||||||||||||||||||||||||||||||||||||  |||||||||||||||
Db   1380  TGGGAGTGGGTTTCACCAGAAGCAGCAGTAGTCTAACCGTAAGGAGGGCGCTTGCCACGGTG  1439

Qy   1454  AGATTCATGACTGG  1467
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Db   1440  AGATTCATGACTGG  1453
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RESULT 14
AX316093
LOCUS   AX316093   1457 bp   DNA   linear   PAT 14-DEC-2001
DEFINITION Sequence 2 from Patent WO0190312.
ACCESSION   AX316093
VERSION   AX316093.1 GI:17899284
KEYWORDS   unidentified
SOURCE   unidentified
  ORGANISM unclassified sequences.
REFERENCE   1
  AUTHORS   Hovanec,T.A. and Burrell,P.C.
  TITLE   Ammonia-oxidizing bacteria
  JOURNAL   Patent: WO 0190312-A 2 29-NOV-2001;
            AQUARIA, INC. (US)
FEATURES   Location/Qualifiers
     source   1..1457
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="AOB Type A1 ammonia-oxidizing bacterium represented
                     by R7 clone187"
ORIGIN

Query Match   92.6%; Score 1358.8; DB 6; Length 1457;
Best Local Similarity   97.2%; Pred. No. 2e-16;
Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

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Qy    16  ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTGCAC  75
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Db     1  ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTGCAT  60

Qy    76  CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAAGTGTCCAGAAGTGGGGGATA  135
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Db    61  CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAAGTGTCCAGAAGAGGGGGGTA  120

Qy   136  ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA  195
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Db   121  ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTAAGGAGGAAAGCAGGGGATCGAAA  180

Qy   196  ACGCATCGAAAGATGTGCTAATACCGCATATACTCTAAGGAGGAAAGCAGGGGATCGAAA  255
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Db   181  GACCTTGGCTTTGGGGGCCCAAGGTTGGGTAAGTTGGGGTTAAGTTGGGGTTAAGGCCTAC  240

Qy   256  CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  315
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Db   241  CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  300

Qy   316  GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC  375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC  360

Qy   376  CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAGA  434
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Db   1440 AGATTCATGACTGG 1453

RESULT 15
LOCUS   AF386757
DEFINITION AF386757   1457 bp   DNA   linear   ENV 10-MAY-2004
            Nitrosomonas sp. R7c187 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF386757
VERSION   AF386757.1 GI:17864834
KEYWORDS   ENV.
SOURCE   Nitrosomonas sp. R7c187
  ORGANISM Nitrosomonas sp. R7c187
            Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
            Nitrosomonadaceae; Nitrosomonas; environmental samples.
REFERENCE   1 (bases 1 to 1457)
  AUTHORS   Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
  TITLE   Identification of bacteria responsible for ammonia oxidation in
            freshwater aquaria
  JOURNAL   Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
  PUBMED   11722936
REFERENCE   2 (bases 1 to 1457)
  AUTHORS   Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
  TITLE   Direct Submission
  JOURNAL   Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria
            Group, 6100 Condor Dr, Moorpark, CA 93021, USA
FEATURES   Location/Qualifiers
     source   1..1457
                     /organism="Nitrosomonas sp. R7c187"
                     /mol_type="genomic DNA"
                     /isolation_source="ammonia-oxidizing bacteria isolated
                     from freshwater aquaria enrichments"
                     /db_xref="taxon:180512"
                     /clone="R7c187"
                     /environmental_sample
     rRNA   <1..>1457
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ORIGIN

Query Match   92.5%;   Score 1357.2;   DB 3;   Length 1457;
Best Local Similarity 97.2%; Pred. No. 2.2e-16;
Matches 1413; Conservative   0; Mismatches 38; Indels   3; Gaps   3;

Qy   16 ATTGAACGCTGCGGCATGCTTACACATGCAAGTCAAGTCAAGCGCAGCACGGGTGCTTGCAC   75
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Db   1 ATTGAACGCTGCGGCATGCTTACACATGCAAGTCAAGTCAAGCGCAGCACGGGTGCTTGCAT   60

Qy   76 CTGGTGGCGAGTGGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA 135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTGGTGGCGAGTGGGCGGACGGGTGAGTAATGCATCGGAACGTATCCGGAAGAGGGGGATA 120

Qy   136 ACGCATCGAAAGATGTGCTAATACCGCCATATTCTTCTACGGGAAAGCAGGGGATCGAAA 195
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Db   121 ACGCATCGAAAGATGTGCTAATACCGCCATATACTCTAAGGAAAGCAGGGGATCGAAA 180

Qy   196 GACCTTGTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GACCTTGCGCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAAGCCTAC 240

Qy   256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 300

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 360

Qy   376 CAGCAATGCCGCGTGAGTGAAGAAG--CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 434
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   361 CAGCAATGCCGCGTGAGTGAAGAAGGCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 420

Qy   435 AAAGGTTGTGACTAATAATCACAACTTATGATGTGACCGACAGAAGCACCGGCTAAC 494
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Db   421 AAAGGTTACGGTAAATAATCGTGACCCATGACGAATCGACAGAAGCACCGGCTAAC 480

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Qy    495  TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  554
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Db    481  TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  540

Qy    555  AAAGGGTGCGCAGGCGGCCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT  614
           ||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Db    541  AAAGGGTGCGCAGGCGGCCTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT  600

Qy    615  TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAATTCCATGTGTAGCAG  674
           ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db    601  TGCGTTTGAAACTACAAAGCTAGAGTGTGGCAGAGGGAGGTGGAATTCCATGTGTAGCAG  660

Qy    675  TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACT  734
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACT  720

Qy    735  GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGTCCACGCC  794
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGTCCACGCC  780

Qy    795  CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGTAGCTAACGCGTGA  854
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    781  CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCTTGGTAACGTAGCTAACGCGTGA  840

Qy    855  AGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGAATTGACGGGGACCC  914
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  AGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGAATTGACGGGGACCC  900

Qy    915  GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  974
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Db    901  GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  960

Qy    975  GACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT  1034
           |||||||||||||||   |||||||||||| |||||| ||||||||||||||||||||||
Db    961  GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC--TTCGGGAACGCTAACACAGGTGCT  1019

Qy    1035 GCATGGCTGTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC  1094
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Db    1020 GCATGGCTGTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC  1079

Qy    1095 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC  1154
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Db    1080 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC  1139

Qy    1155 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA  1214
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA  1199

Qy    1215 ATACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGCGC  1274
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 ATACAATGGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGCGC  1259

Qy    1275 GTCGTAGTCCGGATCGGATCGGAGTCTTGCAACTCGACTCCGTGAAGTCGGATAATCGCTAGTAATCG  1334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1260 GTCGTAGTCCGGATCGGATCGGAGTCTTGCAACTCGACTCCGTGAAGTCGGATAATCGCTAGTAATCG  1319

Qy    1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCA  1394
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA  1379

Qy    1395 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGGCG  1453
           ||||||||||||||||||||||||||||||||||||     ||||||||||||||||||||
Db    1380 TGGGAGTGGGTTTCACCAGAAGCAGTCTAACCGTAAGGAGGGCGTTTGCCACGGTG  1439

Qy    1454 AGATTCATGACTGG  1467
           ||||||||||||||
Db    1440 AGATTCATGACTGG  1453
```

Search completed: April 6, 2006, 21:24:45
Job time : 7274 secs

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OM nucleic - nucleic search, using sw model

```
              GenCore version 5.1.7
    Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

Run on: April 6, 2006, 19:12:36 ; Search time 936 Seconds
                        (without alignments)
                        10445.624 Million cell updates/sec

Title: US-10-659-983A-18
Perfect score: 1467
Sequence: 1 ttgatcatggctcagatga.........acggcgagattcatgactgg 1467

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 496997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_21:*
     1: geneseqm1980s:*
     2: geneseqm1990s:*
     3: geneseqm2000s:*
     4: geneseqm2001as:*
     5: geneseqm2001bs:*
     6: geneseqm2002as:*
     7: geneseqm2002bs:*
     8: geneseqm2003as:*
     9: geneseqm2003bs:*
    10: geneseqm2003cs:*
    11: geneseqm2003ds:*
    12: geneseqm2004as:*
    13: geneseqm2004as:*
    14: geneseqm2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1467	100.0	1467	12	ADM32721	Adm32721 AOB P4clo
2	1440.2	98.2	1491	12	ADM32723	Adm32723 AOB BF16c
3	1403.4	95.7	1494	12	ADM32722	Adm32722 AOB P4clo
4	1358.8	92.6	1457	6	ABA02416	Aba02416 Type A am
5	1358.8	92.6	1457	6	ADM32704	Adm32704 AOB Type
6	1357.2	92.5	1457	12	ABA02417	Aba02417 Type A1 a
7	1357.2	92.5	1457	12	ADM32705	Adm32705 AOB Type
8	1252	85.3	1458	6	ABA02418	Aba02418 Type B am
9	1252	85.3	1458	12	ADM32706	Adm32706 AOB Type
10	1210.6	82.5	1460	6	ABA02419	Aba02419 Type C am
11	1210.6	82.5	1460	12	ADM32707	Adm32707 AOB Type
12	1189.8	81.1	1495	6	ABQ78660	Abq78660 Nucleotid
13	1189	81.0	1485	6	AAC86030	Aac86030 16s rDNA,
14	1171.2	79.8	1460	4	AAC86026	Aac86026 16s rDNA,
15	1170.2	79.8	1530	13	ADR45500	Adr45500 R.tenuis
16	1162.8	79.3	1460	4	AAC86024	Aac86024 R.tenuis
17	1151.8	78.5	1459	4	AAC86028	Aac86028 16s rDNA,
18	1150.4	78.4	1464	6	ABL40355	Abl40355 Sequence
19	1145.2	78.1	1460	4	AAC86022	Aac86022 R. tenuis
20	1144.2	78.0	1460	4	AAC86021	Aac86021 R. tenuis
21	1144.2	78.0	1526	2	AAT01866	Aat01866 P.cepacia
22	1141.2	77.8	1478	4	AAC86023	Aac86023 R. purpur
23	1132.2	77.2	1535	2	AAV24295	Aav24295 Burkholde
24	1132.2	77.2	1535	10	ADB61689	Adb61689 16S rRNA
25	1131.8	77.2	1532	2	AAQ26729	Aaq26729 16S rRNA
26	1131.8	77.2	1532	10	ADB61686	Adb61686 16S rRNA
27	1130.4	77.1	1426	4	AAC86029	Aac86029 16s rDNA,
28	1128.2	76.9	1530	14	ADW12666	Adw12666 Variovora
29	1120.6	76.4	1532	4	AAQ64008	Aaq64008 16S rRNA
30	1116.8	76.1	1464	10	ADB61688	Adb61688 16S rRNA
31	1113.2	75.9	1485	10	ADB61687	Adb61687 16S rRNA
32	1110.2	75.7	1509	12	ADQ67895	Adq67895 Acidovora
33	1108.6	75.6	1509	12	ADQ67894	Adq67894 Acidovora
34	1106.2	75.4	1610	10	ADB61691	Adb61691 16S rRNA
35	1104.2	75.3	1400	8	ABZ69298	Abz69298 J lividum
36	1104	75.3	1536	2	AAT18765	Aat18765 Pseudomon
37	1103.4	75.2	1452	6	ABV72366	Abv72366 Nucleotid
38	1103.4	75.2	1496	12	ADQ16355	Adq16355 Nucleotid
39	1103.4	75.2	1496	14	AEA01071	Aea01071 Bordetell
40	1102.6	75.2	1400	8	ABZ69299	Abz69299 J lividum
41	1102.2	75.1	1482	8	ABZ69304	Abz69304 Janthinob
42	1102	75.1	1463	10	ADC53929	Adc53929 Phenyl hy
43	1101.6	75.1	1544	10	ADB61693	Adb61693 16S rRNA
44	1101.6	75.1	110000	3	AAA81490_00	Aaa81490 N. mening
45	1101.6	75.1	110000	3	AAA81490_02	Continuation (3 of

ALIGNMENTS

```
RESULT 1
ADM32721
ID   ADM32721 standard; DNA; 1467 BP.
XX
AC   ADM32721;
XX
DT   17-JUN-2004  (first entry)
XX
DE   AOB P4clone42 16S rDNA.
XX
KW   16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW   aqueous environment; freshwater; seawater; aquarium; ss.
XX
OS   Nitrosomonas aestuarii.
XX
PN   WO2004026772-A2.
XX
PD   01-APR-2004.
XX
PF   10-SEP-2003; 2003WO-US028210.
XX
PR   19-SEP-2002; 2002US-0386217P.
PR   19-SEP-2002; 2002US-0386218P.
PR   19-SEP-2002; 2002US-0386219P.
XX
PA   (AQUA-) AQUARIA INC.
XX
PI   Hovanec TA;
XX
DR   WPI; 2004-304936/28.
XX
PT   New composition comprising an isolated bacterial strain that oxidizes
PT   ammonia to nitrite, useful for alleviating or preventing the accumulation
PT   of ammonia in aqueous environment.
XX
PS   Claim 1; Page 13; 98pp; English.
XX
CC   This sequence represents a 16S rDNA sequence derived from an ammonia
CC   oxidising bacteria (AOB). This sequence may be used in a composition
CC   which comprises an isolated bacterial strain that oxidizes ammonia to
CC   nitrite. The composition may be used for alleviating or preventing the
CC   accumulation of ammonia in a medium. The ammonia is reduced by at least
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CC    30% when compared with a level of ammonia that would exist in the absence
CC    of the bacterial strain. The composition is useful for alleviating or
CC    preventing the accumulation of ammonia in aqueous environment, e.g. a
CC    freshwater or seawater aquarium.
XX
SQ    Sequence 1467 BP; 384 A; 320 C; 451 G; 312 T; 0 U; 0 Other;

Query Match       100.0%;  Score 1467;  DB 12;  Length 1467;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1467;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1  TTGATCATGGTCAGATTGAACGCTGGCGGCATGTCTTACACATGCAAGTCGAACGGCAG    60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  TTGATCATGGTCAGATTGAACGCTGGCGGCATGTCTTACACATGCAAGTCGAACGGCAG    60

Qy     61  CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTC   120

Qy    121  CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA   180

Qy    181  AGCAGGGGATCGAAAGACCTTGTCGCTTGCGGCGGACGGGTGAGTCCTGATTAGCTAGTTGGT   240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  AGCAGGGGATCGAAAGACCTTGTCGCTTGCGGCGGACGGGTGAGTCCTGATTAGCTAGTTGGT   240

Qy    241  GGGTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC   300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GGGTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC   300

Qy    301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTGGACAATG   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTGGACAATG   360

Qy    361  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCT   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCT   420

Qy    421  TTCAGTCGGAGAGAAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAG   480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TTCAGTCGGAGAGAAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAG   480

Qy    481  AAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCG   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCG   540

Qy    541  GAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGG   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GAATTACTGGGCGTAAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGG   600

Qy    601  CTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAAT   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAAT   660

Qy    661  TCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCC   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCC   720

Qy    721  CCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCC   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCC   780

Qy    781  TGGTAGTCCACGCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACG   840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TGGTAGTCCACGCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACG   840

Qy    841  TAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGA   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGA   900

Qy    901  ATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAA   960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  ATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAA   960

Qy    961  CCTTACCTACCCTTGACATGTGAGCGGAATATTTAGAGATAAAATAGTGCCTTCGGGAACG  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  CCTTACCTACCCTTGACATGTGAGCGGAATATTTAGAGATAAAATAGTGCCTTCGGGAACG  1020

Qy   1021  CTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  CTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC  1080

Qy   1081  GCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAAGTTGGGCACTTTAATGAGACT  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  GCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAAGTTGGGCACTTTAATGAGACT  1140

Qy   1141  GCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTA  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTA  1200

Qy   1201  GGGCTTCACACGTAATACAATGGGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTA  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  GGGCTTCACACGTAATACAATGGGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTA  1260

Qy   1261  ATCTCAGAAAGCCGGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  ATCTCAGAAAGCCGGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGA  1320

Qy   1321  ATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACAC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACAC  1380

Qy   1381  CGCCCGTCACACCATGGGAGTGGGTTCACCAGAAGCAGTAGTCTAACCGTAAGGGC  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CGCCCGTCACACCATGGGAGTGGGTTCACCAGAAGCAGTAGTCTAACCGTAAGGGGC  1440

Qy   1441  GTTTGGCCACGGCGAGATTCATGACTGG  1467
           ||||||||||||||||||||||||||||
Db   1441  GTTTGGCCACGGCGAGATTCATGACTGG  1467
```

```
RESULT 2
ADM32723
ID   ADM32723 standard; DNA; 1491 BP.
XX
AC   ADM32723;
XX
DT   17-JUN-2004  (first entry)
XX
DE   AOB BF16clone57 16S rDNA.
XX
KW   16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW   aqueous environment; freshwater; seawater; aquarium; ss.
XX
OS   Nitrosomonas aestuarii.
XX
XX
PN   WO2004026772-A2.
XX
PD   01-APR-2004.
XX
PF   10-SEP-2003; 2003WO-US028210.
XX
PR   19-SEP-2002; 2002US-0386217P.
PR   19-SEP-2002; 2002US-0386218P.
PR   19-SEP-2002; 2002US-0386219P.
XX
PA   (AQUA-) AQUARIA INC.
XX
PI   Hovanec TA;
XX
DR   WPI; 2004-304936/28.
XX
PT   New composition comprising an isolated bacterial strain that oxidizes
PT   ammonia to nitrite, useful for alleviating or preventing the accumulation
PT   of ammonia in aqueous environment.
```

```
XX
PS   Claim 1; Page 15; 99pp; English.
XX
CC   This sequence represents a 16S rDNA sequence derived from an ammonia
CC   oxidising bacteria (AOB). This sequence may be used in a composition
CC   which comprises an isolated bacterial strain that oxidizes ammonia to
CC   nitrite. The composition may be used for alleviating or preventing the
CC   accumulation of ammonia in a medium. The ammonia is reduced by at least
CC   30% when compared with a level of ammonia that would exist in the absence
CC   of the bacterial strain. The composition is useful for alleviating or
CC   preventing the accumulation of ammonia in aqueous environment, e.g. a
CC   freshwater or seawater aquarium.
XX
SQ   Sequence 1491 BP; 392 A; 323 C; 457 G; 319 T; 0 U; 0 Other;

Query Match     98.2%;  Score 1440.2;  DB 12;  Length 1491;
Best Local Similarity   99.7%;  Pred. No. 0;
Matches 1464;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    2;

Qy      1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG 62

Qy     61 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTC 122

Qy    121 CAGAAGTGGGGGATAACGTATCGAAAGATGTCTAATACCGCATATTCTCTACGGAGGAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 CAGAAGTGGGGGATAACGTATCGAAAGATGTCTAATACCGCATATTCTCTACGGAGGAA 182

Qy    181 AGCAGGGGATGAAAGACCTTGTCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 AGCAGGGGATGAAAGACCTTGTCTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT 242

Qy    241 GGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 GGGTAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC 302

Qy    301 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 362

Qy    361 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAG-CTTCGGGTTGTAAAGCTC 419
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    363 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTC 422

Qy    420 TTTCAGTTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 TTTCAGTTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA 482

Qy    480 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 542

Qy    540 GGAATTACTGGGCGTAAAGGCGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGG 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 GGAATTACTGGGCGTAAAGGCGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGG 602

Qy    600 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGCAGCAGAGGGGGGTGGAA 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGCAGCAGAGGGGGGTGGAA 662

Qy    660 TTCCATGTGTAGCAGTGAAATGCGTAGAGATCGATGGCGAAGGCAGCC 719
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    663 TTCCATGTGTAGCAGTGAAATGCGTAGAGATCGATGGCGAAGGCAGCC 722

Qy    720 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    723 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 782

Qy    780 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    783 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC 842

Qy    840 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTGACGGTCGCAGGATTAAAACTCAAAGG 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    843 GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTGACGGTCGCAGGATTAAAACTCAAAGG 902

Qy    900 AATTGACGGGGACCCGCACAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    903 AATTGACGGGGACCCGCACAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA 962

Qy    960 ACCTTACCTACCCTTGACATGGTCGAATATTTAGAGATAAAATAGTGCCTTCGGGAAC 1019
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    963 ACCTTACCTACCCTTGACATGGTCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1022

Qy   1020 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1023 GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1082

Qy   1080 CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATCATTTAGTTGGGCACTTTAATGAGAC 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1083 CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATCATTTAGTTGGGCACTTTAATGAGAC 1142

Qy   1140 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1143 TGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT 1202

Qy   1200 AGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCCGCGAGGGGGAGCT 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1203 AGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCCGCGAGGGGGAGCT 1262

Qy   1260 AATCTCAGAAAGCGCGTCGTAGTCCGGATCAGCATGTCGCGGTGAGTCGCGAGTCGG 1319
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1263 AATCTCAGAAAGCGCGTCGTAGTCCGGATCAGCATGTCGCGGTGAGTCGCGAGTCGG 1322

Qy   1320 AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1323 AATCGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACA 1382

Qy   1380 CCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGCAGATAGTCTAACCGTAA-GAGG 1438
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1383 CCGCCCGTCACCATGGGAGTGGGTTTCACCAGAAGCAGCAGATAGTCTAACCGTAACCGGAG 1442

Qy   1439 GCGTTTGCCACGGCGAGATTCATGACTGG 1467
          |||||||||||||||||||||||||||||
Db   1443 GCGTTTGCCACGGCGAGATTCATGACTGG 1471
```

```
RESULT 3
ADM32722
ID   ADM32722 standard; DNA; 1494 BP.
XX
AC   ADM32722;
XX
DT   17-JUN-2004  (first entry)
XX
DE   AOB P4clone31 16S rDNA.
XX
KW   16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW   aqueous environment; freshwater; seawater; aquarium; ss.
XX
OS   Nitrosomonas aestuarii.
XX
PN   WO2004026772-A2.
XX
PD   01-APR-2004.
XX
PF   10-SEP-2003;  2003WO-US028210.
XX
PR   19-SEP-2002;  2002US-0386217P.
PR   19-SEP-2002;  2002US-0386218P.
PR   19-SEP-2002;  2002US-0386219P.
XX
PA   (AQUA-) AQUARIA INC.
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Db   664  TTCCATGTGTTAGCAGTGAAATGCGTAGAGATGATGGAGGAACATCGATGGCGAAGGCAGCC  723

Qy   720  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAAACAGGATTAGATACC  779
Db   724  CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAAACAGGATTAGATACC  783

Qy   780  CTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC  839
Db   784  CTGGTAGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAAC  843

Qy   840  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  899
Db   844  GTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG  903

Qy   900  AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  959
Db   904  AATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAA  963

Qy   960  ACCTTACCTACCCTTGACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAAC  1019
Db   964  ACCTTACCTACCCTTGACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAAC  1023

Qy  1020  GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1079
Db  1024  GCTAACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1083

Qy  1080  CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTTAGTTGGGCACTTTAATGAGAC  1139
Db  1084  CGCAACGAGCGCAACCCTTGTCATTAATTGCCATCATTTAGTTGGGCACTTTAATGAGAC  1143

Qy  1140  TGCCCGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT  1199
Db  1144  TGCCCGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGT  1203

Qy  1200  AGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT  1259
Db  1204  AGGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCT  1263

Qy  1260  AATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGG  1319
Db  1264  AATCTCAGAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGG  1323

Qy  1320  AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACA  1379
Db  1324  AATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACA  1383

Qy  1380  CCGCCCGTCACACCATGGGAGTGGGTTCACCAGAAGCAGATAGTCTAACCGT-AAGAGG  1438
Db  1384  CCGCCCGTCACACCATGGAAGTGGGTTGGTCGCTGCACCAGAAGTAGGTTGTCTAACCCTCGGGAGG  1443

Qy  1439  GCGTTTGCCACGGCGAGATTCATGACTGG  1467
Db  1444  ACGCTTACCACGGTGTGGTCAATGACTTG  1472
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RESULT 4
ABA02416

CC   This sequence represents a 16S rDNA sequence derived from an ammonia
CC   oxidising bacteria (AOB). This sequence may be used in a composition
CC   which comprises an isolated bacterial strain that oxidizes ammonia to
CC   nitrite. The composition may be used for alleviating or preventing the
CC   accumulation of ammonia in a medium. The ammonia is reduced by at least
CC   30% when compared with a level of ammonia that would exist in the absence
CC   of the bacterial strain. The composition is useful for alleviating or
CC   preventing the accumulation of ammonia in aqueous environment, e.g. a
CC   freshwater or seawater aquarium.
XX

SQ   Sequence 1494 BP; 392 A; 327 C; 459 G; 316 T; 0 U; 0 Other;

Query Match   95.7%;   Score 1403.4;   DB 12;   Length 1494;
Best Local Similarity 98.1%;   Pred. No. 0;
Matches 1441;   Conservative   0;   Mismatches   26;   Indels   2;   Gaps   2;

```
Qy    1  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG  60
Db    4  TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAG  63

Qy   61  CACGGGTGCTTGCACCTGGTGGCGAGTGCGCGACGGGTGAGTAATGCATCGGAACGTGTC  120
Db   64  CACGGGTGCTTGCACCTGGTGGCGAGTGCGCGACGGGTGAGTAATGCATCGGAACGTGTC  123

Qy  121  CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATACGCCCTACGGGGAA  180
Db  124  CGGAAGTGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATACGGCCCTACGGGGAA  183

Qy  181  AGCAGGGGATCGCAAAGACCTTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT  240
Db  184  AGCAGGGGATCGCAAAGACCTTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGT  243

Qy  241  GGGGTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  300
Db  244  GGGGTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACAC  303

Qy  301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG  360
Db  304  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAACG  363

Qy  361  GGGGAAAGCCTGATCCAGCCATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTC  419
Db  364  GGGCAAAGCCTGATCCAGCCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTC  423

Qy  420  TTTCAGTCGGAAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA  479
Db  424  TTTCAGTCGGAAGAAGAAAGGTTGTGACTAATAATCACAACTTATGACGGTACCGACAGAA  483

Qy  480  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  539
Db  484  GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC  543

Qy  540  GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTTGTAAGTCAGATGTGAAATCCCCGG  599
Db  544  GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTTGTAAGTCAGATGTGAAATCCCCGG  603

Qy  600  GCTTAACCTGGGAATTGCGTTTGAAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA  659
Db  604  GCTTAACCTGGGAATTGCGTTTGAAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA  663

Qy  660  TTCCATGTGTAGCAGTGAAATGCGTAGAGATGATGGAGGAACATCGATGGCGAAGGCAGCC  719
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XX
PD   29-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-US016265.
XX
PR   19-MAY-2000; 2000US-00573684.
XX
PA   (AQUA-) AQUARIA INC.
XX
PI   Hovanec TA, Burrell PC;
XX
DR   WPI; 2002-075367/10.
XX
PT   New bacteria capable of oxidising ammonia to nitrite, for preventing or
PT   alleviating the accumulation of ammonia in fresh water aquaria, seawater
PT   aquaria and waste water.
XX
PS   Claim 2; Page 5; 62pp; English.
XX
CC   The invention relates to 4 novel types of ammonia-oxidising bacteria
CC   (AOB) found in freshwater aquaria. The bacteria are able to oxidise
CC   ammonia to nitrite and are members of the ammonia-oxidising bacteria
CC   family of the beta subdivision of Proteobacteria. The 4 types of bacteria
CC   can de distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
CC   sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
CC   R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
CC   C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
CC   gene sequences of the ammonia-oxidising bacteria of the invention,
CC   oligonucleotide probes and primers for the detection of these bacteria,
CC   and compositions comprising the bacteria. The bacteria of the invention
CC   are useful in biological filters for reducing ammonia accumulation in
CC   both freshwater and seawater aquaria. They may also be used in waste
CC   water treatment and in bioremediation processes to reduce the level of
CC   pollution caused by ammonia. The present sequence represents R7clone140,
CC   a 16S rRNA gene sequence from the type A ammonia-oxidising bacterium of
CC   the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 1457 BP; 378 A; 315 C; 456 G; 308 T; 0 U; 0 Other;

Query Match             92.6%;  Score 1358.8;  DB 6;  Length 1457;
Best Local Similarity   97.2%;  Pred. No. 0;
Matches 1414;  Conservative  0;  Mismatches  37;  Indels  3;  Gaps  3;

Qy        16 ATTGAACGCTGGCGGCGATGCTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTGCAC 75
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db         1 ATTGAACGCTGCGCGGCATGCTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTGCAT 60

Qy        76 CTGGTGGCGAGTGCCGACGGGTGAGTAATGCATCCGAAGTGTCCAGAAGTGGGGGGATA 135
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CTGGTGGCGAGTGCCGACGGGTGAGTAATGCATCCGAAGTGTCCAGAAGTGGGGGGTA 120

Qy       136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 195
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTAAGGAGGAAAGCAGGGGATCGAAA 180

Qy       196 GACCTTGCGCTTTTGGAGCGGCCGATGCCGTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GACCTTGCGCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 240

Qy       256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 315
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 300

Qy       316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC 360

Qy       376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGGAAGA 434
             |||||||||||||||||||||||||| |||||||||| ||||||||||||||||||||||
Db       361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGGAAGA 420

Qy       435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC 494
             ||||||  |  ||||||  ||| | | |||| ||| ||||||||||||||||||||||
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Db       421 AAAGGTTACGGTGAAATAATCGTGACTCATGACGTATCGACAGAAGAAGCACCGGCTAAC 480
             |||||||                                 ||||||||||||||||||||
Qy       495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGTTAATTACTGGGCGT 554
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGTTAATTACTGGGGCGT 540

Qy       555 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 614
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 600

Qy       615 TGCGTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAATTCCATGTGTAGCAG 674
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 TGCGTTTGAAACTACACAAGGCTAGAGTGTGGCAGAGGGGGTGGAATTCCATGTGTAGCAG 660

Qy       675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCTGGGGTTAACACT 734
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCTCTGGGGTTAACACT 720

Qy       735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 794
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 780

Qy       795 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGCTAGCTAACGCGTGA 854
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGCTAGCTAACGCGTGA 840

Qy       855 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 914
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 900

Qy       915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 974
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 960

Qy       975 GACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC-TTCGGGAACGCTAACACAGGTGCT 1019

Qy      1035 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1020 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1079

Qy      1095 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1154
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1080 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1139

Qy      1155 GGAGGAAGGTGGGGATGACGTCAAGTCCTCAGTCCTATGGTGGGTTAGGGCTTCACACGTA 1214
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCAGTCCCTATGGTGGGTTAGGGCTTCACGTA 1199

Qy      1215 ATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAAGCGC 1274
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1200 ATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAAGCGC 1259

Qy      1275 GTCGTAGTCCGATCGGATTGCGAGTCTGCGAGTCTGCAACTGCACTCCGGTGAAGTCGGAATCG 1334
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1260 GTCGTAGTCCGATCGGATTGCGAGTCTGCGAGTCTGCAACTGCACTCCGGTGAAGTCGGAATCG 1319

Qy      1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1379

Qy      1395 TGGGAGTGGGTTTCACCAGAAGCAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGGCG 1453
             ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db      1380 TGGGAGTGGGTTTCACCAGAAGCAGCAGGTAGTCTAACCGTAAGGGGGCGTTGCCACGGTG 1439

Qy      1454 AGATTCATGACTGG 1467
             ||||||||||||||
Db      1440 AGATTCATGACTGG 1453
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RESULT 5
ADM32704

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ID   ADM32704 standard; DNA; 1457 BP.
XX
AC   ADM32704;
XX
DT   17-JUN-2004  (first entry)
XX
DE   AOB Type A R7clone140 16S rDNA.
XX
KW   16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW   aqueous environment; freshwater; seawater; aquarium; ss.
OS   Nitrosomonas sp.
XX
PN   WO2004026772-A2.
XX
PD   01-APR-2004.
XX
PF   10-SEP-2003; 2003WO-US028210.
XX
PR   19-SEP-2002; 2002US-0386217P.
PR   19-SEP-2002; 2002US-0386218P.
PR   19-SEP-2002; 2002US-0386219P.
XX
PA   (AQUA-) AQUARIA INC.
XX
PI   Hovanec TA;
XX
DR   WPI; 2004-304936/28.
XX
PT   New composition comprising an isolated bacterial strain that oxidizes
PT   ammonia to nitrite, useful for alleviating or preventing the accumulation
PT   of ammonia in aqueous environment.
XX
PS   Disclosure; Page 8-9; 98pp; English.
XX
CC   This sequence represents a 16S rDNA sequence derived from an ammonia
CC   oxidising bacteria (AOB). This sequence may be used in a composition
CC   which comprises an isolated bacterial strain that oxidizes ammonia to
CC   nitrite. The composition may be used for alleviating or preventing the
CC   accumulation of ammonia in a medium. The ammonia is reduced by at least
CC   30% when compared with a level of ammonia that would exist in the absence
CC   of the bacterial strain. The composition is useful for alleviating or
CC   preventing the accumulation of ammonia in aqueous environment, e.g. a
CC   freshwater or seawater aquarium.
XX
SQ   Sequence 1457 BP; 378 A; 315 C; 456 G; 308 T; 0 U; 0 Other;

Query Match             92.6%;  Score 1358.8;  DB 12;  Length 1457;
Best Local Similarity   97.2%;  Pred. No. 0;
Matches 1414;  Conservative    0;  Mismatches   37;  Indels    3;  Gaps    3;
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```
Qy       16 ATTGAACGCTGGCGGCATGCTTTACACGCAGTCGAACGGCAGCAGCGGGGGATGGCTTGCAC   75
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATTGAACGCTGGCGGCATGCTTTACACGCAGTCGAACGGCAGCAGCGGGGGATGGCTTGCAT   60

Qy       76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCCGGAACGTGTCCAGAAGTGGGGGATA  135
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCCGGAACGTATCCAGAAGAGGGGGGTA  120

Qy      136 ACGCATCGAAAGATGTCTAATACCGCATATTCTTCTACGGAGGAAAAGCAGGGGATCGAAA  195
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ACGCATCGAAAGATGTCTAATACCGCATATACTTAAGGAGGAAAAGCAGGGGATCGAAA  180

Qy      196 GACCTTGTGCTTTTGGAGCGGCCGATGCGGGTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC  255
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GACCTTGCGCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC  240

Qy      256 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  315
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG  300

Qy      316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGGAAGCCTGATC  375
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGGAAGCCTGATC  360
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Db      301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGGAAGCCTGATC  360
Qy      376 CAGCAATGCGCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA  434
            |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db      361 CAGCAATGCGCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA  420

Qy      435 AAAGGTTGTGACTAATACAACTCATGATGTACCGACAGAAGAAGCACCGGCTAAC  494
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AAAGGTTACGGTAAATAATCGTCATCATGACGCGTATCGACAGAAGAAGCACCGGCTAAC  480

Qy      495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  554
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT  540

Qy      555 AAAGGGTGCGCAGGCGGCTTGTTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT  614
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 AAAGGGTGCGCAGGCGGCTTGTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT  600

Qy      615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG  674
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TGCGTTTGAAACTACAAGCTAGAGTGTGCGAGAGGAGGAGTGGAATTCCATGTGTAGCAG  660

Qy      675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTTAACACT  734
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCTCCTGGGTTAACACT  720

Qy      735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  794
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  780

Qy      795 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGTAGCTAACGCGTGA  854
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCTTGGTAACGTAGCTAACGCGTGA  840

Qy      855 AGTTGACCGCCTGGGGAGTACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGGACCC  914
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC  900

Qy      915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT  974
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAAACCTTACCTACCCTT  960

Qy      975 GACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGACGCTAACACAGTGCTGCT 1034
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db      961 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC-TTCCGGAACGCTAACACAGTGCT  1019

Qy     1035 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1020 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC  1079

Qy     1095 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC  1154
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1080 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC  1139

Qy     1155 GGAGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGGCTTCACACGTA 1214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1140 GGAGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGGCTTCACACGTA  1199

Qy     1215 ATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1274
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1200 ATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC  1259

Qy     1275 GTCGTAGTCCGGATCGCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCG  1334
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1260 GTCGTAGTCCGGATCGCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCG  1319

Qy     1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA  1379

Qy     1395 TGGGAGTGGGTTTCACCAGAAGCAGGTAGTCTAACCCTAA-GAGGGCGTTTGCCACGGCG 1453
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     1380 TGGGAGTGGGTTTCACCAGAAGCAGGTAGTCTAACCCTAAGGAGGGGCGTTTGCCACGGCG  1439
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Qy   1454 AGATTCATGACTGG 1467
           |||||||||||||
Db   1440 AGATTCATGACTGG 1453

RESULT 6
ABA02417
ID   ABA02417 standard; DNA; 1457 BP.
XX
AC   ABA02417;
XX
DT   29-AUG-2003 (revised)
DT   04-MAR-2002 (first entry)
XX
DE   Type A1 ammonia-oxidising bacterium 16S rRNA gene sequence, R7clone187.
XX
KW   Type A1; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;
KW   ribosomal RNA; aquarium; aquaculture; waste water treatment;
KW   bioremediation; ds.
XX
OS   Nitrosomonadales.
XX
PN   WO200190312-A1.
XX
PD   29-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-US016265.
XX
PR   19-MAY-2000; 2000US-00573684.
XX
PA   (AQUA-) AQUARIA INC.
XX
PI   Hovanec TA, Burrell PC;
XX
DR   WPI; 2002-075367/10.
XX
PT   New bacteria capable of oxidizing ammonia to nitrite, for preventing or
PT   alleviating the accumulation of ammonia in fresh water aquaria, seawater
PT   aquaria and waste water.
XX
PS   Claim 2; Page 6; 62pp; English.
XX
CC   The invention relates to 4 novel types of ammonia-oxidising bacteria
CC   (AOB) found in freshwater aquaria. The bacteria are able to oxidise
CC   ammonia to nitrite and are members of the ammonia-oxidising bacteria
CC   family of the beta subdivision of Proteobacteria. The 4 types of bacteria
CC   can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
CC   sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
CC   R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
CC   C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
CC   gene sequences of the ammonia-oxidising bacteria of the invention,
CC   oligonucleotide probes and primers for the detection of these bacteria,
CC   and compositions comprising the bacteria. The bacteria of the invention
CC   are useful in biological filters for reducing ammonia accumulation in
CC   both freshwater and seawater aquaria. They may also be used in waste
CC   water treatment and in bioremediation processes to reduce the level of
CC   pollution caused by ammonia. The present sequence represents R7clone187,
CC   a 16S rRNA gene sequence from the type A1 ammonia-oxidising bacterium of
CC   the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 1457 BP; 379 A; 317 C; 455 G; 306 T; 0 U; 0 Other;

Query Match   92.5%;   Score 1357.2;   DB 6;   Length 1457;
Best Local Similarity   97.2%;   Pred. No. 0;
Matches 1413;   Mismatches   38;   Conservative   0;   Indels   3;   Gaps   3;

Qy   16 ATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTCGAACGGCAGCGGTGCTTGCAC 75
           ||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCGGTGACGATGCTTGCAT 60

Qy   76 CTGGTGGCGAGTGGCGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGCGTGGGGGATA 135
           ||||| |||||| |||||||||||||||||||||||||||||||||||| |||||| |||||
Db   140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCAGGGCCCTTATGGGTAGGGGCTTCACAGTA 1199

Qy   136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTTCTACGGGAGAAAAGCAGGGGATCGAAA 195
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   121 ACGCATCGAAAGATGTGCTAATACCGCATATACTCTAAGGAGGAAAAGCAGGGGATCGAAA 180

Qy   196 GACCTTGCTGCTTTTGGAGCGGCCGATGCGTCAGTGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   181 GACCTTGCTGCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 240

Qy   256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 315
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 300

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 360

Qy   376 CAGCAATGCCGCGTGAGTGAAGAAG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 434
           |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db   361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 420

Qy   435 AAAGGTTGTGACTAATATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAC 494
           |||||| |||| ||||| |||| |||||||||||||||||||||||||||||||||||||
Db   421 AAAGGTTACGGTAAAATAATCGTGACCCATGACGTATCGACAGAAGAAGCACCGGCTAAC 480

Qy   495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 540

Qy   555 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 614
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 600

Qy   615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGAATTCCATGTGTAGCAG 674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGCGTTTGAAACTACAAAGCTAGAGTGTGGCAGAGGGGAGTGAATTCCATGTGTAGCAG 660

Qy   675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTAACACT 734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTAACACT 720

Qy   735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 794
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 780

Qy   795 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGACGTAACGCGTGA 854
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CTAAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCTTGGTAACGAGCTAACGCGTGA 840

Qy   855 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 914
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 900

Qy   915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAACCTTACCTACCCTT 974
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 960

Qy   975 GACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACAGGTGCT 1034
           |||||| |||| |||||||||||||||| ||||| ||||||||||||||||||||| |||
Db   961 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC-TTCGGGAACGCTAACAGGTGT 1019

Qy   1035 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1079

Qy   1095 CCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1154
           ||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   1080 CCTTGTCATTAATTGCCATCATTTGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1139

Qy   1155 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGCGTAGGGCTTCACAGTA 1214
           ||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||||||
Db   1140 GGAGGAAGGTGGGGATGACGTCAAGTCCTCAGGGCCCTTATGGGTAGGGGCTTCACAGTA 1199

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                                    Matches 1413;  Conservative   0;  Mismatches  38;  Indels   3;  Gaps   3;

                                    Qy      16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGGTGCTGCAC   75
                                               ||||||||||||||||||||||||||||||||||||||  |||||||||||||||
                                    Db       1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGATGCTTGCAT   60

                                    Qy      76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA   135
                                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db      61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGGTA   120

                                    Qy     136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA   195
                                               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     121 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA   180

                                    Qy     196 GACCTTGTGCTTTTGGAGCGGCCGATGCCGATTAGCTAGTTGGTGGGGTAAAGGCCTAC   255
                                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     181 GACCTTGCGCTTTTGGAGCGGCCCGATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC   240

                                    Qy     256 CAAGGCAACGATCACGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG   315
                                               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG   300

                                    Qy     316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC   375
                                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     301 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATC   360

                                    Qy     376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGGGAAGA   434
                                               ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
                                    Db     361 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGTCGGGAAGA   420

                                    Qy     435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC   494
                                               ||||||  |||||||||||||||||     ||  |||||||||||||||||||||||||||
                                    Db     421 AAAGGTTACGGTAAATAATCGTGACCCATGACCATCGACAGAAGAAGCACCGGCTAAC   480

                                    Qy     495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT   554
                                               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     481 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT   540

                                    Qy     555 AAAGGGTGCGCAGGCGGTTTGTAAGTCAGATGTGAAATCCCGGGGCTTAACCTGGGAAT   614
                                               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     541 AAAGGGTGCGCAGGCGGTTTGTAAGTCAGATGTGAAATCCCGGGGCTTAACCTGGGAAT   600

                                    Qy     615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG   674
                                               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     601 TGCGTTTGAAACTACAAAGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCATGTGTAGCAG   660

                                    Qy     675 TGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCCCCCTGGGTAACACT   734
                                               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     661 TGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCCCTCCTGGGTAACACT   720

                                    Qy     735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC   794
                                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     721 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC   780

                                    Qy     795 CTAACGATGTCAACTAGTTGTTGGGCCTTACTAGGCTTGGTAACGGCTAACGCGTGA   854
                                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     781 CTAACGATGTCAACTAGTTGTTGGGCCTTATTAGGCTTGGTAACGGCTAACGCGTGA   840

                                    Qy     855 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC   914
                                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     841 AGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC   900

                                    Qy     915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT   974
                                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     901 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT   960

                                    Qy     975 GACATGTAGCGAATATTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGTGCT   1034
                                               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db     961 GACATGTAGCGAATTTTCTAGAGATAGAATAGTAGTGC-TTCGGGAACCAACAGTGCT   1019

                                    Qy    1035 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC   1094
                                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                    Db    1020 GCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC   1079
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Qy    1215 ATACAATGGGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAAGCC   1274
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 ATACAATGGGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAAGCGC   1259

Qy    1275 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG   1334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1260 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG   1319

Qy    1335 CGGATCAGCATGTCGGGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA   1394
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA   1379

Qy    1395 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGGCG   1453
           ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db    1380 TGGGAGTGGGTTTCACCAGAAGCAGCAGTAGTCTAACCGTAACCGTAAGGAGGGCGCTTGCCACGGTG   1439

Qy    1454 AGATTCATGACTGG   1467
           |||||||||||||
Db    1440 AGATTCATGACTGG   1453
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RESULT 7
ADM32705
ID   ADM32705 standard; DNA; 1457 BP.
XX
AC   ADM32705;
XX
DT   17-JUN-2004 (first entry)
XX
DE   AOB Type A1 R7clone187 16S rDNA.
XX
KW   16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW   aqueous environment; freshwater; seawater; aquarium; ss.
XX
OS   Nitrosomonas sp.
XX
PN   WO2004026772-A2.
XX
PD   01-APR-2004.
XX
PF   10-SEP-2003; 2003WO-US028210.
XX
PR   19-SEP-2002; 2002US-0386217P.
PR   19-SEP-2002; 2002US-0386218P.
PR   19-SEP-2002; 2002US-0386219P.
XX
PA   (AQUA-) AQUARIA INC.
XX
PI   Hovanec TA;
XX
DR   WPI; 2004-304936/28.
XX
PT   New composition comprising an isolated bacterial strain that oxidizes
PT   ammonia to nitrite, useful for alleviating or preventing the accumulation
PT   of ammonia in aqueous environment.
XX
PS   Disclosure; Page 10; 98pp; English.
XX
CC   This sequence represents a 16S rDNA sequence derived from an ammonia
CC   oxidising bacteria (AOB). This sequence may be used in a composition
CC   which comprises an isolated bacterial strain that oxidizes ammonia to
CC   nitrite. The composition may be used for alleviating or preventing the
CC   accumulation of ammonia in a medium. The ammonia is reduced by at least
CC   30% when compared with a level of ammonia that would exist in the absence
CC   of the bacterial strain. The composition is useful for alleviating or
CC   preventing the accumulation of ammonia in aqueous environment, e.g. a
CC   freshwater or seawater aquarium.
XX
SQ   Sequence 1457 BP; 379 A; 317 C; 455 G; 306 T; 0 U; 0 Other;

Query Match   92.5%;   Score 1357.2;   DB 12;   Length 1457;
Best Local Similarity 97.2%;   Pred. No. 0;

CC   R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
CC   C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
CC   gene sequences of the ammonia-oxidising bacteria of the invention,
CC   oligonucleotide probes and primers for the detection of these bacteria,
CC   and compositions comprising the bacteria. The bacteria of the invention
CC   are useful in biological filters for reducing ammonia accumulation in
CC   both freshwater and seawater aquaria. They may also be used in waste
CC   water treatment and in bioremediation processes to reduce the level of
CC   pollution caused by ammonia. The present sequence represents R3clone5, a
CC   16S rRNA gene sequence from the type B ammonia-oxidising bacterium of the
CC   invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 1458 BP; 368 A; 342 C; 466 G; 282 T; 0 U; 0 Other;

Query Match   85.3%;   Score 1252;   DB 6;   Length 1458;
Best Local Similarity 93.1%;   Pred. No. 0;
Matches 1355;   Conservative   0;   Mismatches   95;   Indels   6;   Gaps   4;

Qy   16 ATTGAACGCTGGCGCAGTGCCATGCTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTGCAC 75
              ||||||||||||||||||||||| |||||||||||||||||||||||||| |||||||||||||
Db   1 ATTGAACGCTGGCGCAGTGCCATGCTTACACATGCAAGTCGAACGGCAGCGGCGGGGC--AACC 58

Qy   76 CTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGGTGTCCAGAAGTGGGGGATA 135
              ||||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||
Db   59 CTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACGTATCTTCGAGGGGGGGATA 118

Qy   136 ACGGATCGAAAGATGTGCTAATACCGCATATTCCTACGGAGAAAGCAGGGGATCGAAA 195
              |||| ||||| ||| || ||||||||||||||| |||||||||||||||||||||||||
Db   119 ACGCACCGAAAGGTGTGCTAATACCGCATAATCTCCACGGAGAAAGCAGGGGATCGCAA 178

Qy   196 GACCTTGTGCTTTTGGAGCGGCCGATGCCGATTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
              ||||||||||||| |||||||||||||||||||||| |||||||||||||||||||||||||||
Db   179 GACCTTGCGCTCTTGGAGCGGCCGATGTCGATTGATTAGCTAGTTGGTGGGGTGAGTAATGCTTAC 238

Qy   256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGAACGGCCAGCCACACTGGGACTGAGACACG 315
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   239 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 298

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCAAAGCCTGATC 375
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   299 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGGAAACCCTGATC 358

Qy   376 CAGCAATGCGCGTGAGTGAAGAAG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAGA 434
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   359 CAGCCATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGCCGGAACGA 418

Qy   435 AAAGGTTGTGACTAATAATCACAACTTATGATGTACCGACAGAAGAAGCACCGGCTAAC 494
              |||| || ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   419 AACGGTCACGCTAATACCCGTGACTACTGACCTACTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACAC...GCTAAC 478

Qy   495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   479 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 538

Qy   555 AAAGGGTGCGCAGGCGGCTTGTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGAAT 614
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   539 AAAGCGTGCGCAGGCGGTTTGTAAGTCAGATGTGAAAGCCCCGGGCTTAACCTGGGAAC 598

Qy   615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG 674
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   599 TGCGTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCACGTGTAGCAG 658

Qy   675 TGAAATGCGTAGAGATATGGAAGGAACAATCGATGGCGAAGGCAGCCCCCTGGGTAACACT 734
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   659 TGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCAGCCCCCTGGGTAACACC 718

Qy   735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 794
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   719 GACGCTCAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC 778

Qy   795 CTAAACGATGTCAACTAGTTGTTGTTGGCCTTACTAGGCTTGGTAACGTAACGCGCGTGA 854
              ||||||||||||||||||||| |||||||||||||||||||||||||||| |||||||||||
Db   779 CTAAACGATGTCAACTAGTTGTTGTCGGGTCTTTAACGGACTTGGTAACGCAGCTAACGCGTGA 838

Qy   1095 CCTTGTCATTAATTGCCATCATTTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1154
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 CCTTGTCATTAATTGCCATCATTTGGTTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1139

Qy   1155 GGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 GGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGCGCCCTTATGGGTAGGGCTTCACACGTA 1199

Qy   1215 ATACAATGGCCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGGCGC 1274
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   1200 ATACAATGGCCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGGCGC 1259

Qy   1275 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG 1334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG 1319

Qy   1335 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 CGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1379

Qy   1395 TGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACGGTAA-GAGGGCGGTTGCCACGGCG 1453
              ||||||||||||||||||||||||||||| |||||||||| |||||||||||||||||||
Db   1380 TGGGAGTGGGTTTCACCAGAAGCAGGTAGTCTAACCGTAACCGTAAGGAGGGGGCTTGCCACGGTG 1439

Qy   1454 AGATTCATGACTGG 1467
              ||||||||||||||
Db   1440 AGATTCATGACTGG 1453

RESULT 8
ABA02418
ID   ABA02418 standard; DNA; 1458 BP.
XX
AC   ABA02418;
XX
DT   29-AUG-2003 (revised)
DT   04-MAR-2002 (first entry)
XX
DE   Type B ammonia-oxidising bacterium 16S rRNA gene sequence, R3clone5.
XX
KW   Type B; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;
KW   ribosomal RNA; aquarium; aquaculture; waste water treatment;
KW   bioremediation; ds.
OS   Nitrosomonadales.
XX
PN   WO200190312-A1.
XX
PD   29-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-US016265.
XX
PR   19-MAY-2000; 2000US-00573684.
XX
PA   (AQUA-) AQUARIA INC.
XX
PI   Hovanec TA, Burrell PC;
XX
DR   WPI; 2002-075367/10.
XX
PT   New bacteria capable of oxidizing ammonia to nitrite, for preventing or
PT   alleviating the accumulation of ammonia in fresh water aquaria, seawater
PT   aquaria and waste water.
XX
PS   Claim 2; Page 7; 62pp; English.
XX
CC   The invention relates to 4 novel types of ammonia-oxidising bacteria
CC   (AOB) found in freshwater aquaria. The bacteria are able to oxidise
CC   ammonia to nitrite and are members of the ammonia-oxidising bacteria
CC   family of the beta subdivision of Proteobacteria. The 4 types of bacteria
CC   can de distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
CC   sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,

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PI   Hovanec TA;
XX
DR   WPI; 2004-304936/28.
XX
PT   New composition comprising an isolated bacterial strain that oxidizes
PT   ammonia to nitrite, useful for alleviating or preventing the accumulation
PT   of ammonia in aqueous environment.
XX
PS   Disclosure; Page 11; 98pp; English.
XX
XX
CC   This sequence represents a 16S rDNA sequence derived from an ammonia
CC   oxidising bacteria (AOB). This sequence may be used in a composition
CC   which comprises an isolated bacterial strain that oxidizes ammonia to
CC   nitrite. The composition may be used for alleviating or preventing the
CC   accumulation of ammonia in a medium. The ammonia is reduced by at least
CC   30% when compared with a level of ammonia that would exist in the absence
CC   of the bacterial strain. The composition is useful for alleviating or
CC   preventing the accumulation of ammonia in aqueous environment, e.g. a
CC   freshwater or seawater aquarium.
XX
SQ   Sequence 1458 BP; 368 A; 342 C; 466 G; 282 T; 0 U; 0 Other;

Query Match      85.3%;   Score 1252;   DB 12;   Length 1458;
Best Local Similarity     93.1%;   Pred. No. 0;
Matches 1355;   Conservative   0;   Mismatches   95;   Indels   6;   Gaps   4;

Qy     16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCAGCGGCACGGTGCTTGCAC 75
          |||||||||||||||||||||||||||||||||||||||||||||||||||        |   ||
Db      1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCAGCGGGC--AACC 58

Qy     76 CTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTCCAGAACGTGTTCGAGGTGGGGGATA 135
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db     59 CTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTCCAGAACGTGTATCTTCGAGGGGGGGGATA 118

Qy    136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA 195
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    119 ACGCACCGAAAGGTGTGCTAATACCGCATAATCTCCACGGAGGAAAAGCAGGGGATCGCAA 178

Qy    196 GACCTTGCTTTTGGAGCGGCCGATGCGTCCGATTAGCTAGTTGGTGGGGTAAAGGCCTAC 255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    179 GACCTTGCTTCTTGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGTAATGGCCTAC 238

Qy    256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 315
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG 298

Qy    316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGGGAAACCCTGATC 358

Qy    376 CAGCAATGCCGCGTGAGTGAAGAAG--CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 434
          |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db    359 CAGCCATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCAGCCGGAACGA 418

Qy    435 AAAGGTTGTGACTAATAATCACAACTTATGATGTACGACAGAAGAAGCACCGGCTAAC 494
          ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 AACGGTCACGGCGGTAATACCCGTGACTACTGACGCTACTGACGGGAAGAAGCACCGGCTAAC 478

Qy    495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT 538

Qy    555 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT 614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 AAAGCGTGCGCAGGCGGTTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAC 598

Qy    615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCATCGTGTAGCAG 674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 TGCGTTTGAAACTACAAAGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCACGTGTAGCAG 658

Qy    675 TGAAATGCGTAGAGATATGGAAGAACATGCATGGCGAAGGCAGCCCCCTGGGGTTAACACT 734
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 TGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCAGCCCCCTGGGGTTAACACC 718

Qy    855 AGTTGCACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 914
          ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 AGTTGGCCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 898

Qy    915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 974
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    899 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 958

Qy    975 GACATGTAGCGGAATATTTAGAGATAAAATAGTGCC--TTCGGGACAACGCTAACACAGTG 1032
          |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db    959 GACATGTACCGAAGCCCGCGAGAGTGGGTGCCCGAAAAGGGAGCGGTAACACAGCAGGTG 1018

Qy   1033 CTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1092
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 CTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1078

Qy   1093 ACCCTTGTCATTAATTGCCATCATTCAGTTGGGCACTTTAATGACACTGCCGGTGACAAA 1152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 ACCCTTGTCATTAATTGCCATCATTCAGTTGGGCACTTTAATGAACTGCCGGTGACAAA 1138

Qy   1153 CCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGTAGGCTTCACACG 1212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 CCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGTAGGCTTCACACG 1198

Qy   1213 TAATACAATGGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGC 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 TAATACAATGGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGC 1258

Qy   1273 GCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAAT 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1259 GCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAAT 1318

Qy   1333 CGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCGTCACAC 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1319 CGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACAC 1378

Qy   1393 CATGGGAGTGGGTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCACGG 1451
          |||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db   1379 CATGGGAGTGGGTTCACCAGAAGCAGGTAGTCTAACCGCCAAGGAGGGGGCCGCTTGCCACGG 1438

Qy   1452 CGAGATTCATGACTGG 1467
          |||||||||||||||||
Db   1439 TGAGATTCATGACTGG 1454
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RESULT 9

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ADM32706
ID   ADM32706 standard; DNA; 1458 BP.
XX
AC   ADM32706;
XX
DT   17-JUN-2004  (first entry)
XX
DE   AOB Type B R3clone5 16S rDNA.
XX
KW   16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW   aqueous environment; freshwater; seawater; aquarium; ss.
XX
OS   Nitrosomonas sp.
XX
XX
PN   WO2004026772-A2.
XX
PD   01-APR-2004.
XX
PR   10-SEP-2003; 2003WO-US028210.
XX
PR   19-SEP-2002; 200US-0386217P.
PR   19-SEP-2002; 2002US-0386218P.
PR   19-SEP-2002; 2002US-0386219P.
XX
PA   (AQUA-) AQUARIA INC.
.XX
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PD   29-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-US016265.
XX
PR   19-MAY-2000; 2000US-00573684.
XX
PA   (AQUA-) AQUARIA INC.
XX
PI   Hovanec TA, Burrell PC;
XX
DR   WPI; 2002-075367/10.
XX
PT   New bacteria capable of oxidizing ammonia to nitrite, for preventing or
PT   alleviating the accumulation of ammonia in fresh water aquaria, seawater
PT   aquaria and waste water.
XX
PS   Claim 2; Page 8; 62pp; English.
XX
CC   The invention relates to 4 novel types of ammonia-oxidising bacteria
CC   (AOB) found in freshwater aquaria. The bacteria are able to oxidise
CC   ammonia to nitrite and are members of the ammonia-oxidising bacteria
CC   family of the beta subdivision of Proteobacteria. The 4 types of bacteria
CC   can de distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
CC   sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
CC   R7clone140), type A1 (e.g., R7clone18), and type B (e.g., R3clone5) and type
CC   C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
CC   gene sequences of the ammonia-oxidising bacteria of the invention,
CC   oligonucleotide probes and primers for the detection of these bacteria,
CC   and compositions comprising the bacteria. The bacteria of the invention
CC   are useful in biological filters for reducing ammonia accumulation in
CC   both freshwater and seawater aquaria. They may also be used in waste
CC   water treatment and in bioremediation processes to reduce the level of
CC   pollution caused by ammonia. The present sequence represents R3clone47, a
CC   16S rRNA gene sequence from the type C ammonia-oxidising bacterium of the
CC   invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 1460 BP; 388 A; 316 C; 454 G; 302 T; 0 U; 0 Other;

Query Match   82.5%; Score 1210.6; DB 6; Length 1460;
Best Local Similarity   92.5%; Pred. No. 0;
Matches 1350; Conservative   0; Mismatches   99; Indels   10; Gaps   7;

Qy   16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCGGGTGCTTGCAC 75
            |||||||||||||||||||||||||||||||||||||||||||| ||||||| ||||
Db   1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG--CGGGGGCTTCGGC 58

Qy   76 CTGGTGGGCGGACTGGCGGACACGGGTGAGTAATGCATCGGAAGTGTTCCAGAAGTGGGGGATA 135
            ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   59 CTGCCGGGCGGACTGGCGACGGGTGCGCAACGGGTGAGTAATACATCGGAACGTGTCCTTAAGTGGGGAATA 118

Qy   136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAAGCAGGGGATCGAAA 195
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 ACGCATCGAAAGATGTGCTAATACCGCATA-TCTCTGAGGAGAAAAGCAGGGGATCGCAA 177

Qy   196 GACCTTGTCCTTTGGAGCGGCCCGATGGCCCGATGTCCGATGTCTGATTAGCTAGTTGGTGGGG 255
            |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   178 GACCTTGCCTAAAGGAGCGGCCCGATGTCCGATGTCTGATTAGCTAGTTGGTGGGG 237

Qy   256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGATCAGCCACACTGGGACTGAGACACG 315
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCACACTGGGACTGAGACACG 297

Qy   316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 375
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC 357

Qy   376 CAGCAATGCGCGTGAGTGAAGAGG--CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 434
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   358 CAGCCATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCGGTTGTGAAAGA 417

Qy   435 AAAGGTTGTGACTAATAATCACAACTTATGATGTTACCGACAGAAGAAGCACCGGCTAAC 494
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   418 AAGAATCATGATGAATAATTATGATTTTATGACGGTACTGACAGAAAAGCACCGGCTAAC 477

Qy   735 GACGCTCATGCACGAAAGCGTGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCACGCC 794
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   719 GACGCTCAGGCACGAAAGCGTGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCACGCC 778

Qy   795 CTAAACGATGTCAACTAGTTGTTGGGCTTGGGCCTTACTAGGCTTGGTAACGTAGTCCGTGA 854
            ||||||| |||||||||||| | |||||| |||||||||||||||||||||||||
Db   779 CTAAACGATGTCAACTAGTTGTTCGGTCTTAACGACTTGGTAACGTAGTCCGTGA 838

Qy   855 AGTTGACCGCCTGGGGAGTACGGTCGCAGGATTAAAACTCAAAGGAATTGACGGGACCC 914
            ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   839 AGTTGGGCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCC 898

Qy   915 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 974
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   899 GCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTT 958

Qy   975 GACATGTAGCGAATATTTTAGAGATAAAATAGTGCC--TTCGGGAACGCTAACACAGTG 1032
            |||||| |||| |||| ||||||||||||||||||||
Db   959 GACATGTACCGAAGCCCGCCAGAGGTGGGTGTGCCCGAAAGGGAGCGGTAACACAGTG 1018

Qy   1033 CTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCGCAACGAGCGCA 1092
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 CTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCGCAACGAGCGCA 1078

Qy   1093 ACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTAATGAGACTGCCGGTGACAAA 1152
            ||||||||||||||| |||||||||||||||||||| |||||||||||||||||||||
Db   1079 ACCCTTGTCATTAATTGCCATCATTCAGTTGGGCACTTAATGAGACTGCCGGTGACAAA 1138

Qy   1153 CCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGTAGGGCTTCACACG 1212
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 CCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGTAGGGCTTCACACG 1198

Qy   1213 TAATACAATGGGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGC 1272
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 TAATACAATGGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGC 1258

Qy   1273 GCGTCGTAGTCCGGATCGGAGTCTGCAACTCCGTGAAGTCGGAATCGCTAGTAAT 1332
            ||||||||||||||||||||||||||||||||||||||||||
Db   1259 GCGTCGTAGTCCGGATCGGAGTCTGCAACTCCGTGAAGTCGGAATCGCTAGTAAT 1318

Qy   1333 CCGGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACAC 1392
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1319 CGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACAC 1378

Qy   1393 CATGGGAGTGGGTTTCACCAGAAGTAGGTAGATAGTCTAAACGTAA-GAGGGCGTTTGCCACGG 1451
            ||||||||||||||||||||||||||||| | ||||| |||||||||||||||||
Db   1379 CATGGGAGTGGGTTTCACCAGAAGTAGGTAGTCTAACCGCAGGAGGACGAGGGCGCTGCCACGG 1438

Qy   1452 CGAGATTCATGACTGG 1467
            ||||||||||||||||
Db   1439 TGAGATTCATGACTGG 1454

RESULT 10
ABA02419
ID   ABA02419 standard; DNA; 1460 BP.
XX
AC   ABA02419;
XX
DT   29-AUG-2003   (revised)
DT   04-MAR-2002   (first entry)
XX
DE   Type C ammonia-oxidising bacterium 16S rRNA gene sequence, R3clone47.
XX
KW   Type C; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;
KW   ribosomal RNA; aquarium; aquaculture; waste water treatment;
KW   bioremediation; ds.
XX
OS   Nitrosomonadales.
XX
PN   WO200190312-A1.
XX

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XX
AC   ADM32707;
XX
DT   17-JUN-2004  (first entry)
XX
DE   AOB Type C R5clone47 16S rDNA.
XX
KW   16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW   aqueous environment; freshwater; seawater; aquarium; ss.
XX
OS   Nitrosomonas sp.
XX
PN   WO2004026772-A2.
XX
PD   01-APR-2004.
XX
PF   10-SEP-2003; 2003WO-US028210.
XX
PR   19-SEP-2002; 2002US-0386217P.
PR   19-SEP-2002; 2002US-0386218P.
PR   19-SEP-2002; 2002US-0386219P.
XX
PA   (AQUA-) AQUARIA INC.
PI   Hovanec TA;
XX
DR   WPI; 2004-304936/28.
XX
PT   New composition comprising an isolated bacterial strain that oxidizes
PT   ammonia to nitrite, useful for alleviating or preventing the accumulation
PT   of ammonia in aqueous environment.
XX
PS   Disclosure; Page 12; 98pp; English.
XX
CC   This sequence represents a 16S rDNA sequence derived from an ammonia
CC   oxidising bacteria (AOB). This sequence may be used in a composition
CC   which comprises an isolated bacterial strain that oxidizes ammonia to
CC   nitrite. The composition may be used for alleviating or preventing the
CC   accumulation of ammonia in a medium. The ammonia is reduced by at least
CC   30% when compared with a level of ammonia that would exist in the absence
CC   of the bacterial strain. The composition is useful for alleviating or
CC   preventing the accumulation of ammonia in aqueous environment, e.g. a
CC   freshwater or seawater aquarium.
XX
SQ   Sequence 1460 BP; 388 A; 316 C; 454 G; 302 T; 0 U; 0 Other;

Query Match             82.5%;  Score 1210.6;  DB 12;  Length 1460;
Best Local Similarity   92.5%;  Pred. No. 0;
Matches 1350;    Conservative    0;  Mismatches   99;  Indels   10;  Gaps   7;
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Qy          16 ATTGAACGCTGCGGCGCATGCTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTCGCAC    75
               |||||||||||||||||||||||||||||||| |||||||||||||||| |          |
Db           1 ATTGAACGCTGCGGCGCATGCTTACACATGCAAGTCGAACGGCAG--CGGGGGCTTCGGC   58

Qy          76 CTGGTGGCGAGTGGCGCGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTGGGGGATA   135
               |||                  || ||||||||||||||||||||| |||||||||||||||
Db          59 CTGCCGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTCCTTAAGTGGGGGAATA   118

Qy         136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGGATCGAAA   195
               |||||||||||||||||||||||||||||| |||||||||| |
Db         119 ACGCATCGAAAGATGTGCTAATACCGCATA-TCTCTGAGGAGGAAAAGCAGGGGATCGCAA   177

Qy         196 GACCTTGTCTTTGGAGCGGCGATGCCTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC   255
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 GACCTTGCGCTAAAGGAGCGGCCGATGCGTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC   237

Qy         256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG   315
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         238 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACCACACTGGGACTGAGACACG   297

Qy         316 GCCCAGACTCCTCACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC   375
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         298 GCCCAGACTCCTCACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC   357
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Qy         495 TACGTGGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT   554
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         478 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCGT   537

Qy         555 AAAGGGTGCGCAGGCGGCGTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT   614
               |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db         538 AAAGGGTGCGCAGGCGGCGTTTTGTAAGTGCAGATGTGAAAGCCCCGGGCTTAACCTGGGAAT   597

Qy         615 TGCGTTTGAAACTACAAAGCTAGAGTGTGAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG   674
               |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         598 TGCGTTTGAAACTACAAGCTAGAGTGCACGAGAGGGGAGTGGAATTCCATGTGTAGCAG   657

Qy         675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCTGGGCTTAACACT   734
               |||||||||||||| |||||||||||||||||||||||||||||||||| |||| ||||||
Db         658 TGAAATGCGTAGAGATGTGGAAGAACAACCAGTGGCGAAGGCAGCCTCCCTGGGTTGACACT   717

Qy         735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGTCCACGCC   794
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         718 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGTCCACGCC   777

Qy         795 CTAAACGATGTCAACTAGTTGTTGGGCCTTACTA--GGCTTGGTAACGTAGCTAACGCGT   852
               ||||||||||||||||||||  ||    || || |  ||||||| ||||||||||||||||
Db         778 CTAAACGATGTCAACTGGTTGTTCGGATCTAATTAAGGATTTGGTAACGTAGCTAACGCGT   837

Qy         853 GAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGAC   912
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         838 GAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGAC   897

Qy         913 CCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCC   972
               ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         898 CCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCC   957

Qy         973 TTGACATGTAGGCGAATATTTAGAGATAAAAGTGCC--TTCGGGAACGCTAACACAGG   1030
               ||||||||| |  |  ||           || |||||    ||||||||||||||||||
Db         958 TTGACATGCTTGAAATCGTAGAGATACATAAGAGTGCCGCGAAAAGGGAGCCAAGACACAGG   1017

Qy        1031 TGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCG   1090
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1018 TGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCG   1077

Qy        1091 CAACCCTTGTCATTAATTGCCATCATT--TAGTTGGGCACTTTAATGAGACTGCCGGTGAC   1149
               ||||||||||||||||||||||||||||  || |||||||| || ||||||||||||||||
Db        1078 CAACCCTTGTCACTAATTGCTATCATTCCTAAATGAGCACTTTAGTGAGACTGCCGGTGAC   1137

Qy        1150 AAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCAC   1209
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1138 AAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCAC   1197

Qy        1210 ACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAA   1269
               ||||||||||||||||||||||||| || ||||||||||||||||||||| |||||||||||
Db        1198 ACGTAATACAATGGCGTGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCCAATCTCAGAA   1257

Qy        1270 AGCGCGTCGTAGTCCGGATCGGAGTCTCGCAACTCCGTGAAGTCGGAATCGCTAGT   1329
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1258 AGACGTCGTAGTCCGGATCGGAGTCTCGCAACTCCGTGAAGTCGGAATCGCTAGT   1317

Qy        1330 AATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCA   1389
               ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        1318 AATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCA   1377

Qy        1390 CACCATGGGAGTGGGTTGTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCA   1448
               ||||||||||||||||| |||||||||||||||||||||||||||| |||||||||||||||
Db        1378 CACCATGGGAGTGGGTTGTTTCACCAGAAGCAGGTAGTTTAACCGTAAGGAGGGCGTTTGCCA   1437

Qy        1449 CGGTGGGGGATTCATGACTGG   1467
               || |||||||||||||||||
Db        1438 CGGTGGGGGTCATGACTGG   1456
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RESULT 11
ADM32707    standard; DNA; 1460 BP.
.ID ADM32707
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Qy   1449 CGGCGAGATTCATGACTGG 1467
Db   1438 CGGTGGGGGTCATGACTGG 1456

RESULT 12
ABQ78660
ID   ABQ78660 standard; DNA; 1495 BP.
XX
AC   ABQ78660;
XX
DT   25-NOV-2002 (first entry)
XX
DE   Nucleotide sequence of a fragment of 16S rDNA gene.
XX
KW   16S rDNA; nitrogen oxide; nitrogen; ss.
XX
OS   Denitromonas aromaticus.
XX
PN   JP2002142755-A.
XX
PD   21-MAY-2002.
XX
PF   14-NOV-2000; 2000JP-00346844.
XX
PR   14-NOV-2000; 2000JP-00346844.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (AJIN) AJINOMOTO KK.
XX
DR   WPI; 2002-611517/66.
XX
PT   Microorganism belonging to Denitromonas for removal of nitrogen oxide by
PT   reduction of nitrogen oxide to nitrogen in gas or aqueous solution, has
PT   specific mycological characters.
XX
PS   Disclosure; Page 6-7; 8pp; Japanese.
XX
CC   The present sequence represents a fragment of 16S rDNA gene of
CC   Denitromonas aromaticus. This is a novel microorganism belonging to the
CC   new genus Denitromonas, and which has specific mycological characters.
CC   The new microorganism efficiently reduces and removes nitrogen oxide. The
CC   bacterium is used for the removal of nitrogen oxide. It reduces nitrogen
CC   oxide to nitrogen in a gas or aqueous solution
XX
SQ   Sequence 1495 BP; 363 A; 350 C; 483 G; 299 T; 0 U; 0 Other;

Query Match   81.1%; Score 1189.8; DB 6; Length 1495;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1315; Conservative 0; Mismatches 152; Indels 4; Gaps 3;

Qy   1 TTGATCATGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG   60
Db   1 TTTATCCTGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG   60

Qy   61 CACGGGTGCTTGCACCTGTGGCGAGTGCGGCGGGTGCGCAGTGGTAATGCATCGGAACGTGTC   120
Db   61 CACGGGAGCTTGCTCCTGTGGCGAGTGCGGCGGGTGCGAACGGGTGAGTAATGCATCGGAACGTACC   120

Qy   121 CAGAAGTGGGGGATAACGCATCGGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAA   180
Db   121 CAGTAGTGGGGGATAGTAGGCGAAAGCCGGATTAATACCGCATATTTCCTGAGGAGGAGAA   180

Qy   181 AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGGCCGATGCGCCGATTAGCTAGTTGGT   240
Db   181 AGCGGGGGGGACCTTCGGGCCTCGCGCTACTGGGCGGCGCGATGTGGATTAGCTAGTTGGT   240

Qy   241 GGGTAAAGGCCTACCAAGGCGACGATCAGTAGTTGGTCGTGAGGACGACCACCACAC   300
Db   241 GGGTAAAGGCCTACCAAGGCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACAC   300

Qy   301 TGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTGGACAATG   360

Qy   376 CAGCAATGCCGCGGTGAGTGAAGAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAGA   434
Db   358 CAGCCATGCCGCGGTGAGTGAAGAGGCCTTCGGGTTCGGGTTGTGAGAGCTCTTTTAGTTCAGAAAGA   417

Qy   435 AAAGGTTGTGACTAATAATCACACTTATGATGTGACCGACAGAGAAGCACCGGCTAAC   494
Db   418 AAGAATCATGATGAATAATTATGATTTATGACCGTAACGTAGCTACTGACAGAAAAAGCACCGGCTAAC   477

Qy   495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT   554
Db   478 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCGT   537

Qy   555 AAAGGGTGCGCAGGCGGCTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT   614
Db   538 AAAGGGTGCGCAGGCGGTTTGTAAGTCAGATGTGAAAGCCCCGGGCTTAACCTGGGAAT   597

Qy   615 TGGGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG   674
Db   598 TGGGTTTGAAACTACAAAGCTAGAGTGTGGCAGAGGGGGGTGGAATTCCATGTGTAGCAG   657

Qy   675 TGAAATGCGTAGAGATATGGAAGAACATCGATGCGAAGGCAGCCCCCTGGGTTAACACT   734
Db   658 TGAAATGCGTAGAGATGTGGAAGAACACCGATGCGAAGGCAGCCTCCCTGGGTTGACACT   717

Qy   735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC   794
Db   718 GACCCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC   777

Qy   795 CTAAACGATGTCAACTACTGTGTTGGGCCTTA--GGCTTGGTGAACGTAGCTAACGCGT   852
Db   778 CTAAACGATGTCAACTGGTTGTCGTCGGATCTAATTAAGGATTTTGTAACGTAGCTAACGCGT   837

Qy   853 GAAGTTGACCGCCTGGGGAGTACGGTCCGCAAGGTTAAAACTCAAAGGAATTGACGGGGAC   912
Db   838 GAAGTTGACCGCCTGGGGAGTACGGTCCGCAAGGTTAAAACTCAAAGGAATTGACGGGGAC   897

Qy   913 CCCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCC   972
Db   898 CCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCC   957

Qy   973 TTGACATGCTAGCCGAATATTTTAGAGATAAAATAGTGCC--TTCGGGAACGCTAACACAGG   1030
Db   958 TTGACATGCTTGAATCTGAGAGTAGTGGGTAATAAGCCGAGCATAAGGTGCTGCGGAGCACACAGG   1017

Qy 1031 TGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCG   1090
Db 1018 TGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCG   1077

Qy 1091 CAACCCTTGTCATTAATTGCCATCATT--TAGTTGGGCACTTAATGAGACTGCCGGTGAC   1149
Db 1078 CAACCCTTGTCATTAGTTGCTATCATTCAAATGAGCACTTTAGTGAGACTGCCGGTGAC   1137

Qy 1150 AAACCCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGTGTAGGGCTTCAC   1209
Db 1138 AAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGTGTAGGGCTTCAC   1197

Qy 1210 ACGTAATACAATGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAA   1269
Db 1198 ACGTAATACAATGCGTGTTACAGAGGGTTGCCAACCCGCGAGGGGGAGCCAATCTCAGAA   1257

Qy 1270 AGCGCGTCGTAGTCGGATCGGATTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGT   1329
Db 1258 AGCACGTCGTAGTCGGATCGGATTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGT   1317

Qy 1330 AATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCA   1389
Db 1318 AATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCA   1377

Qy 1390 CACCATGGGAGTGGTTTCACCAGAAGAAGCAGTGGTAA-GAGGGCGTTTGCCA   1448
Db 1378 CACCATGGGAGTGGTTTCACCAGAAGTAGCAGTTTAACCGTAACCGAGGAGGACGCTTGCCA   1437

Db   1381 CACCGCCGTCACCATGGGAGTGGGTTTCACCGAAGTAGTAGTTAACCTTCGGGA 1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1437 GGGCGTTTGCCACGGCGAGATTCATGACTGG 1467

Db   1441 GGGCGCTTACCACGGTGAGATTCATGACTGG 1471

RESULT 13
AAC86030
ID   AAC86030 standard; cDNA; 1485 BP.
XX
AC   AAC86030;
XX
DT   11-SEP-2003 (revised)
DT   29-AUG-2001 (first entry)
XX
DE   16s rDNA, PropEl.
XX
KW   16S rDNA; polyphosphate accumulating organism; PAO; probe; primer;
KW   detection; phosphorus; waste water; sludge; ss.
XX
OS   Propionivibrio pelophilus.
XX
PN   WO20014645 9-A1.
XX
PD   28-JUN-2001.
XX
PF   28-DEC-2000; 2000WO-AU001611.
XX
PR   23-DEC-1999; 99AU-00004867.
XX
PA   (CRCW-) CRC WASTE MANAGEMENT & POLLUTION CONTROL.
XX
PI   Hugenholtz P, Crocetti GR, Tyson GW, Blackall LL;
XX
DR   WPI; 2001-408656/43.
XX
PT   Novel oligonucleotide probe or primer useful for detecting polyphosphate
PT   accumulating organism in a sample, comprises a sequence that is unique to
PT   16S rDNA of polyphosphate accumulating organisms.
XX
PS   Claim 4; Fig 3; 54pp; English.
XX
CC   The sequences given in AAC86021-30 represent 16S rDNA sequences from
CC   polyphosphate accumulating organisms (PAOs). Sequences which are unique
CC   to these 16S rDNA sequences are used to create a probe or primer for
CC   detecting the relevant organisms. The primer/probe sequences are useful
CC   for detecting PAO cells in a sample, by treating cells in the sample to
CC   fix cellular contents, contacting fixed cells with the primer/probe which
CC   is labelled with a radiolabel, a reporter group or a hapten, under
CC   conditions which allow the probe to hybridize with 16S rRNA within the
CC   fixed cell, removing unhybridized probe from the fixed cells, and
CC   detecting the labeled probe-RNA hybrid by fluorescence in situ
CC   hybridization. The primer/probe sequences are useful for identifying PAOs
CC   that are capable of biologically removing phosphorus from waste water.
CC   Rapid assessment of the presence of a number of PAOs in a waste water
CC   sample, can be done using the primer/ probe sequences. They allow quick
CC   and convenient assessment of whether a sludge or waste water sample
CC   includes PAOs and allows quantitation of PAO cells in samples. (Updated
CC   on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 1485 BP; 367 A; 341 C; 482 G; 295 T; 0 U; 0 Other;

Query Match 81.0%; Score 1189; DB 4; Length 1485;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 1319; Conservative 0; Mismatches 140; Indels 6; Gaps 4;

Qy   9 GGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCACGGGTG 68
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCATGGGTG 60

Qy   69 CTTGCACCTGGTGGCGAGTGGGCGACGGGTGAGTAATGCATCGGAACGTGTCCAGAAGTG 128
           ||| ||||||||||||||||||||||||||||||||||||||||||| || ||||||||

Db   301 |||||||||||||||||||||||||||||||||||||||||||||||||
        360 TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG 360

Qy   361 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGATGAAGGC-TTCGGGTTGTAAAGCTC 419
            |||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   361 GGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGATGAAGGCGTAATACGGGGTGTAAAGCTC 420

Qy   420 TTTCAGTCGAGAGAAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAA 479
            |||||||||||| ||| ||| ||||||||||||||||||||||||||||||||||||||
Db   421 TTTCAGTGGTGGAAGAAGAATCATCGCCCCGAATACGGGGGGTGGATGACGGTACCATCAGAA 480

Qy   480 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATC 539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATC 540

Qy   540 GGAATTACTGGGCGTAAAGGCGTAAAGCGTTGTAAGTCAGATGTGAAATCCCCGG 599
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   541 GGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTTGTGTAAGACAGGTGTGAAATCCCCGG 600

Qy   600 GCTTAACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAA 659
            ||||||||||||||| ||| || || ||||||||| ||||| || ||||||||||
Db   601 GCTTAACCTGGGAACTGCGTCTGACGCTGCATGCTAGAGTACGGTGAGAGGGGGGTGGAA 660

Qy   660 TTCCATGTGTAGCAGTGAAATGCGTAGAGATATGGAAGAACATGATGGCGAAGGCAGCC 719
            |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   661 TTCCACGTGTAGCAGTGAAATGCGTAGAGATCGGGGGGAACACCAGTGGCGAAGGCGGCC 720

Qy   720 CCCTGGGTTAACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 779
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   721 CCCTGGGCCTGTACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC 780

Qy   780 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTT--GGGCCTTACTAGGCTTGGTA 837
            |||||||||||||||||||||||||||||||||||||| ||| | ||||| ||||||
Db   781 CTGGTAGTCCACGCCCTAAACGATGTCGACTAGTTGTTCGGAGAGAAACTTCTCGGTA 840

Qy   838 ACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAA 897
            || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ACGCAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAA 900

Qy   898 GGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAA 957
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAA 960

Qy   958 AAACCTTACCTACCCTTGACATGTAGCGGAATATTTAGAGATAAAATAGTGCCTTCGGGA 1017
            |||||||||||| |||||||||| ||||||| ||||||||||||||||||||||||||
Db   961 AAACCTTACCTACCCTTGACAACTGTGAGACATCACTTGGTGCGTCTTCGGGA 1020

Qy   1018 ACGCTACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGT 1077
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCAGACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGT 1080

Qy   1078 CCCGCAACGAGCGCAACCCTTGTCATTAGTTGCCATCATTAGTTGGGACACTTAATGAG 1137
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CCCGCAACGAGCGCAACCCTTGTCATTAGTTGCCACTAATTGAGTTGGGCACTTTAGTGGG 1140

Qy   1138 ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCAAGCCCTTATGG 1197
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCAAGCCCTTATGG 1200

Qy   1198 GTAGGGCTTCACACGTAATACATGGGCCGGTACGGAAGTGCCTACGAGAGGGGGGGGAG 1257
            |||||||||||||||| ||| ||||| ||||||||||||||||||||||||||||||
Db   1201 GTAGGGCTTCACACGTCATACACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAG 1260

Qy   1258 CTAATCTCAGAAAGCCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTC 1317
            | ||| |||||||||||||| ||||||| |||| ||||||||||||||||||||||
Db   1261 CCAATCCCAGAAAGCCGATCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTC 1320

Qy   1318 GGAATCGCTAGTAATCGCGGATCAGCATGTCCGCGGTGAATACGTTCCCGGGTCTTGTACA 1377
            |||| |||||||||| ||||||| |||||||| |||||||||||||||||||||||||||
Db   1321 GGAATCGCTAGTAATCGCGGATCAGCATGTCGGCGGTGAATACGTTCCCGGGTCTTGTACA 1380

Qy   1378 CACCGCCGTCACCATGGGAGTGGGTTTCACCGAAGTAGTAGTTAACCGT-AAGA 1436
            ||| || || |||| ||

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Qy  1204  CTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATC  1263
          ||||||||||||||| ||||||| |||||||||||||||||||||||||||||||| |||||
Db  1201  CTTCACACGTCATCACAATGGTCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCCAATC  1260

Qy  1264  TCAGAAAGCGGCGTCGTAGTCCGATCGGAGTCGCTGCAACTCGACTCCGTGAAGTCGGAATC  1323
          |||||||||| |  |||||||||| | ||||| |||||||||||||| |||||||||||||||
Db  1261  TCAGAAAGCCGATCGTAGTCCGATTGCAGTCTGCAACTCGACTGCATGAAGTCGGAATC  1320

Qy  1324  GCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGC  1383
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  GCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGC  1380

Qy  1384  CCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGGGT  1442
          ||||||||||||||||||| |||| | ||||||||| ||||| |||||||| |||||| |
Db  1381  CCGTCACACCATGGGAGGGGGGTTCTGCCAGAAGTAGGTAGCCTAACCGCAAGGAGGGGGCGC  1440

Qy  1443  TTGCCACGGCGAGATTCATGACTGG  1467
          || |||||| ||| ||||||||||||
Db  1441  TTACCACGCGGGGTTCGTGACTGG  1465


RESULT 14
AAC86026
ID   AAC86026 standard; cDNA; 1460 BP.
XX
AC   AAC86026;
XX
DT   06-AUG-2003  (revised)
DT   29-AUG-2001  (first entry)
XX
DE   16s rDNA, SBRA220.
XX
KW   16S rDNA; polyphosphate accumulating organism; PAO; probe; primer;
KW   detection; phosphorus; waste water; sludge; ss.
XX
OS   Unidentified.
XX
PN   WO200146459-A1.
XX
PD   28-JUN-2001.
XX
PF   28-DEC-2000; 2000WO-AU001611.
PR   23-DEC-1999; 99AU-00004867.
XX
PA   (CRCW-) CRC WASTE MANAGEMENT & POLLUTION CONTROL.
XX
PI   Hugenholtz P, Crocetti GR, Tyson GW, Blackall LL;
XX
DR   WPI; 2001-408656/43.
XX
PT   Novel oligonucleotide probe or primer useful for detecting polyphosphate
PT   accumulating organism in a sample, comprises a sequence that is unique to
PT   16S rDNA of polyphosphate accumulating organisms.
XX
PS   Claim 4; Fig 3; 54pp; English.
XX
CC   The sequences given in AAC86021-30 represent 16S rDNA sequences from
CC   polyphosphate accumulating organisms (PAOs). Sequences which are unique
CC   to these 16S rDNA sequences are used to create a probe or primer for
CC   detecting the relevant organisms. The primer/probe sequences are useful
CC   for detecting PAO cells in a sample, by treating cells in the sample to
CC   fix cellular contents, contacting fixed cells with the primer/probe which
CC   is labelled with a radiolabel, a reporter group or a hapten, under
CC   conditions which allow the probe to hybridize with 16S rRNA within the
CC   fixed cell, removing unhybridized probe from the fixed cells, and
CC   detecting the labeled probe-RNA hybrid by fluorescence in situ
CC   hybridization. The primer/probe sequences are useful for identifying PAOs
CC   that are capable of biologically removing phosphorus from waste water.
CC   Rapid assessment of the presence of a number of PAOs in a waste water
CC   sample, can be done using the primer/ probe sequences. They allow quick
CC   and convenient assessment of whether a sludge or waste water sample
```

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Db    61  CTTGCACCTGATGGCGAGTGGGCGAACGGGTGAGTAATGCATCGGAACGTACCCGGAAGTG  120

Qy   129  GGGGATAACGCATCGGAAAGATGTGCTAATACCGCATATTCTCTACGGAGGAAAGCAGGGG  188
          |||||||||||| ||||   |||| |||||||||||| |  |  || |||  ||||||||||
Db   121  GGGGATAACGTAGCGAAAGTTACGCTAATACCGCATATTCTGTGAGCAGGAAAGAGGGGG  180

Qy   189  ATCGAAAGACCTTGTCGTTTGGAGCGGCCGATGCGTAGTAGTTGGTGGGGTAAA  248
          |||| |||||||| |  || ||||||||||||| || ||||| |||||| |||||
Db   181  ATCGCAAGACCTTCGCTTCGGAGCGGCCGATGTCGGATTAGCTAGTTGGTGGGGTAAA  240

Qy   249  GGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTG  308
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   241  GGCCTACCAAGGCGACGATCCGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTG  300

Qy   309  AGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTGGACAATGGGCGAAAG  368
          |||||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||
Db   301  AGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAG  360

Qy   369  CCTGATCCAGCAATGCCGCGTGAGTGAAGAAG-CTTCGGGTTGTAAAGCTCTTTCAGTC  427
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||
Db   361  CCTGATCCAGCCATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCGGTC  420

Qy   428  GAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGTGTACCGACAAGAAGCACC  487
          ||||||||| |||||||||||||||||||||  |||||||| |||||||||||||||||
Db   421  GGGAAGAAATGGCACGCGTCTAACATAGTGGTTGATGACGGTACCGACCATAAGAAGCACC  480

Qy   488  GGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTAC  547
          |||||||||||||||||||||||||||||||||||||||||||||| || |||||||||||
Db   481  GGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTAC  540

Qy   548  TGGGCGTAAAGGGTGCGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACC  607
          ||||||||||| ||||| || ||||||||| |  | |  |||| |||||||||||| |||||
Db   541  TGGGCGTAAAGGGTGCGTTGCCAGGCGGTTGTGTAAGTCAGATGTGAAATCCCCGGGCTCAACC  600

Qy   608  TGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTAGAATTCCATGT  667
          |||||||||| |||||||||||||||| ||| |||||||||||||||||| ||||||| ||
Db   601  TGGGAATGGCCTTTGAAACTGCACGGCTAGAGTGTGACAGAGGGGGGTAGAATTCCACGT  660

Qy   668  GTAGCAGTGAAATGCGTAGAGATGTGGAGGAACATCATGGCGAAGGCAGCAGCCCCCTGGGT  727
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   661  GTAGCAGTGAAATGCGTAGAGATGTGGAGGAATACCAGTGGCGAAGGCGGCAGCCCCCTGGGT  720

Qy   728  TAACACTGACGGCTCATGCGGCGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGT  787
          |||| ||||||| |||||  ||||||||||||||||||||||||||||||||||||||||||
Db   721  TACTACTGACGCTCATGCGGCGAAAGCGTGGGGAGCAAACAGATTAGATACCCTGGTAGT  780

Qy   788  CCACGCCCTAAACGATGTCAACTAGTTGTTGG--GCCTTACTAGGCTTGGTAACGTAGCT  845
          |||||||||||||||||| |||||||| |||   ||  |||| || |||| ||||| |||
Db   781  CCACGCCCTAAACGATGTCAACTGGTTGTTGGGGAGGGTTAAACCTCTTAGTGTCGTAGCT  840

Qy   846  AACGCGGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGATTAAAACTCAAAGGAATTGA  905
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   841  AACGCGGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGGCTAAAACTCAAAGGAATTGA  900

Qy   906  CGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAAAACCTTA  965
          ||||||||| |||||||| || ||||||||||||||||||||||||||||||||||||||
Db   901  CGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAAAACCTTA  960

Qy   966  CCTACCCTTGACATGTAGCGAATATTTTAGAGATAAAAATAGTGCC--TTCGGGAACGCTA  1023
          ||||||||||||||| || ||||| | ||||||||| || |||||  ||||| |||| ||
Db   961  CCTACCCTTGACATGTCAGGAATCCTTGAGAGATTCCTTAGTGGCCGCAAAGGAGGACTGA  1020

Qy  1024  ACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCA  1083
          |||||||||||||||||||| ||||||||||||||||||| || ||||||||||||||||
Db  1021  ACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCA  1080

Qy  1084  ACGAGCGCAACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGAGACTGCC  1143
          ||||| ||||| ||||||||||||| |||||| |||||||||||||||||||||||||||
Db  1081  ACGAGCGCAACCCTTGTCGTTAATTGCCATCATTAAGTTGGGCACTTTAATGAGACTGCC  1140

Qy  1144  GGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCAGTGGCCCTTATGGGTAGGG  1203
          |||||||||||||||||||||| |||||||||| |||||| ||||||||||||| |||||
Db  1141  GGTGACAAACCCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGG  1200
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CC   includes PAOs and allows quantitation of PAO cells in samples. (Updated
CC   on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 1460 BP; 359 A; 338 C; 475 G; 288 T; 0 U; 0 Other;

Query Match           79.8%;  Score 1171.2;  DB 4;  Length 1460;
Best Local Similarity 90.0%;  Pred. No. 0;
Matches 1312;  Conservative   0;  Mismatches 138;  Indels   8;  Gaps   5;

Qy      16 ATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAGCACGGGTGCTTGCAC    75
           |||| |||||||||||||||| |||||||||||||||||||||||||||||||   ||||
Db       1 ATTAAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGGGGC--AACC    58

Qy      76 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAAGGTGTTCGAGAGTGGGGGATA   135
           ||||||||||||||||||||||||||||||||||||||||| |||  | |||||||||||
Db      59 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTGCCCTGAAGTGGGGGATA   118

Qy     136 ACGCATCGAAAGATGTGCTAATACCGCATATTCTCTACGAGGAAAGCAGGGGATCGAAA   195
           |||||  ||||| | |  |||||||||||||||| | | ||||||||||||||||||| ||
Db     119 ACGCAGCGAAAGCTACGCTAATACCGCATATTCTGTGAGCAGGAAAGCAGGGGATCGCAA   178

Qy     196 GACCTTGTGCTTTGGAGCGGCCGATGCCGTGATTAGCTAGTTGGTGGGGTAAAGGCCTAC   255
           |||||||  |||||| |||||||||| |  ||||||||||||||||||||||| |||||||
Db     179 GACCTTGCGCTTTGGGAGCGGCCGATGTCGGATTAGCTAGTTGGTGGGGTAATGGCCTAC   238

Qy     256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACG   315
           ||||||||||||| ||| | ||||||||||||| || | |||||||||||||||||||||
Db     239 CAAGGCGACGATCCGTAGCCGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACG   298

Qy     316 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATC   375
           ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db     299 GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGGAAGCCTGATC   358

Qy     376 CAGCAATGCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA   434
           ||||||||||||||||||||||||||  |||||||||||||||||||||    | |||||
Db     359 CAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCGGCGGGGAAGA   418

Qy     435 AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC   494
           || |  |||| ||||||| | | |   || || | ||| | ||||||||||||||||||||
Db     419 AATTGCTTGGGTTAATACCCGAGTAGATAGACGTACCCGCAGAAGAAGCACCGGCTAAC   478

Qy     495 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGT   554
           |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db     479 TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCGT   538

Qy     555 AAAGGGTGCGCAGGCGGCTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAT   614
           |||| |||||||||||| ||||||||||||||||||||||||||||| |||||||||||
Db     539 AAAGCGTGCGCAGGCGGTTTTGTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAAC   598

Qy     615 TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCATGTGTAGCAG   674
           ||| ||||| ||| ||||||||||||||||||||||||||||||||||| ||||||||||
Db     599 TGCATTTGAGACTGCAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCACGTGTAGCAG   658

Qy     675 TGAAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGGCAGCCCCCTGGGTAACACT   734
           |||||||||||||||| ||| |||||| ||||||||||||||||||||||||   | ||
Db     659 TGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCAGCCCCCTGGGCCAATACT   718

Qy     735 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC   794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     719 GACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC   778

Qy     795 CTAAACGATGTCAACTAGTTGTTGG--GCCTTACTAGGCTTGGTAACGCTAGCTAACGCGT   852
           ||||||||||||||||||||||||    ||| |||| | ||| || |||||||||||||||
Db     779 CTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCAGCCTTACTAGGCTTGGTAACGCTAGCTAACGCGT   838

Qy     853 GAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGAC   912
           ||||||||||||||||||||||||||||||| || ||||||||||||||||||||||||
Db     839 GAAGTTGACCGCCTGGGGAGTACGGTCGCAAGACTAAAACTCAAAGGAATTGACGGGGAC   898

Qy     913 CCGCACAAGCGGTGGATTATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCC   972
           ||||||||||||||||||| |||| ||||||||||||||||||||||||||||||| |||
Db     899 CCGCACAAGCGGTGGATGTGGATTAATTCCATGCAACGCGAAAAACCTTACCTACCC   958

Qy     973 TTGACATGTGAGGAATAATATTTAGAGATAAATAGTGCCTTC--GGGAACGCTAACACAGG  1030
           |||||||||  ||||| |  | | |||||  || |||| |       |||||| | |||||
Db     959 TTGACATGTCAGGAATCCTGGAGAGATTTGGAGTGCTCGCAAGAGAACGAACCTGACACAGG  1018

Qy    1031 TGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCG  1090
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1019 TGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCG  1078

Qy    1091 CAACCCTTGTCATTAATTGCCATCATTAGTTGGGCACTTTAATGACTGCCGGTGACA  1150
           |||||||||||||| |||||||||||| ||||||||||||||||| |||||||||||
Db    1079 CAACCCTTGTCATTAGTTGCCATCATTCAGTTGGGCACTTTAATGAGACTGCCGGTGACA  1138

Qy    1151 AACCCGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACA  1210
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    1139 AACCCGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACA  1198

Qy    1211 CGTAATACAATGGGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAA  1270
           ||| |||||||||  | ||||||||||||||||||||||||||||||| |||| |||||||
Db    1199 CGTCATACAATGGTCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCCAATCTCAGAAA  1258

Qy    1271 GCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTA  1330
           || | ||||||||||||||| |||||||||||||||| ||||||||||||||||||||||
Db    1259 GCCGATCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTA  1318

Qy    1331 ATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCAC  1390
           |||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db    1319 ATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCCTTGTACACACCGCCCGTCAC  1378

Qy    1391 ACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA-GAGGGCGTTTGCCAC  1449
           ||||||||||  |||||    ||||| || || | ||||| ||  |||||||  | ||||
Db    1379 ACCATGGGAGCGGGTTCTGCCAGAAGTAGTTAGCCTAACCCAAGGAGGGCGGATTACCAC  1438

Qy    1450 GGCGGAGATTCATGACTGG  1467
           |||  || ||| ||||||
Db    1439 GGCAGGGTTCGTGACTGG  1456


RESULT 15
ADR45500
ID   ADR45500 standard; DNA; 1530 BP.
XX
AC   ADR45500;
XX
DT   18-NOV-2004 (first entry)
XX
DE   16S rRNA gene 357f-518r region DNA fragment SeqID89.
XX
KW   357f-518r; 16S rRNA; beta proteobacterium; ammonia oxidising bacteria;
KW   activated sludge; ammonia liquid treatment plant; chemical oxygen demand;
KW   COD; reduction; nitrification; denitrifying; dß.
XX
OS   Unidentified.
XX
PN   JP2004242578-A.
XX
PD   02-SEP-2004.
XX
PF   13-FEB-2003; 2003JP-00035713.
XX
PR   13-FEB-2003; 2003JP-00035713.
XX
PA   (YAWA ) NIPPON STEEL CORP.
XX
DR   WPI; 2004-620179/60.
XX
PT   Novel DNA fragment of microorganisms existing in activated sludge of
PT   ammonia liquid treatment plant, useful as index microorganisms for
PT   evaluating nitrification or denitrifying capability of ammonia liquid.
XX
PS   Claim 45; SEQ ID NO 89; 133pp; Japanese.
XX
CC   This invention relates to a novel DNA fragment comprising the 357f-518r
CC   region of the 16S rRNA gene of beta proteobacteria, belonging to the
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CC   ammonia oxidising bacteria group, or CFB Bacteroides where bacteria
CC   exists in activated sludge of an ammonia liquid treatment plant and used
CC   for chemical oxygen demand (COD) reduction. The invention is useful in
CC   the identification of microorganisms as nitrification or denitrifying
CC   index microorganisms for evaluating the nitrification or denitrifying
CC   capability of ammonia liquid of the activated sludge by fluorescence in
CC   situ hybridisation (FISH). The invention is also useful for developing
CC   apparatus for the processing of ammonia liquid. The DNA fragment enables
CC   evaluation of the nitrification or denitrifying capability of
CC   microorganisms. The present sequence is that of a 16S rRNA gene 357f-518r
XX   region of the invention.
SQ   Sequence 1530 BP; 406 A; 337 C; 474 G; 313 T; 0 U; 0 Other;

Query Match   79.8%;   Score 1170.2;   DB 13;   Length 1530;
Best Local Similarity   91.6%;   Pred. No. 0;
Matches 1350;   Conservative   0;   Mismatches   108;   Indels   15;   Gaps   10;

Qy   5 TCATGGCTCAGATTGAACGCTGGCGGCATGCTTACACATGCAAGTCGAACGGCAGCACG 64
          |||||||||||||||||||||||||||| ||||||| |||||||||||||||| ||
Db   9 TCCTGGCTCAGATTGAACGC-GCGGGCATGCTTACACATGCAAGTCGAACGGCAG--CG 65

Qy   65 GGTGCTTGCACCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGTCCAGA 124
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 GGGGCTTAGGCCTGCCCGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACGTGTCCTTA 125

Qy   125 AGTGGGGGATAACGCATCGAAAGATGTGCTAATACCCGCATATTCTCTACGGAGGAAAGCA 184
          |||||| ||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db   126 AGTGGGGAATAACGCATCGAAAGATGTGCTAATACCGCATA-TCTCTCAGGAGGAAAGCA 184

Qy   185 GGGGATCGAAAGACCTTGCTTTGAGCGGCCGATCGCTGATTAGCTAGTTGGTGGGGG 244
          |||||||||||||||||| ||| ||||||||||||||||||||||||||||||||
Db   185 GGGGATCGCAAGACCTTGCGCTAAAGGAGCGGCCGATGTCTGATTAGCTAGTTGGTGGGGG 244

Qy   245 TAAAGGCCTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCAGCCACACTGGG 304
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245 TAAAGGCCTACCAAGGCAACGATCAGTAGTCTGTCTGAGAGGACGATCAGCCACACTGGG 304

Qy   305 ACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTGGACAATGGGCG 364
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305 ACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCG 364

Qy   365 AAAGCCTGATCCAGCAATGCCGCGTGAGTGATGAAGGCCTTCGGGTTGTAAAGCTCTTTCA 424
          ||||||||||||| ||||| |||||||| ||||||||||||||| ||||||||||||
Db   365 AAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCTTCGGGTTGTAAAGCTCTTTTA 424

Qy   425 GTCGAGAAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACGAGAGAAGC 484
          ||| |||| ||||||| || ||| ||| || |||||||||||||||||||||
Db   425 GTTGGAAAGAAAGAATTATGGTTAATAACTATAATTATGACGGTACCAACAGAAAAAGC 484

Qy   485 ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAAT 544
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   485 ACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAAT 544

Qy   545 TACTGGGCGTAAAGCGTGCGCAGGCGGCCGCTTGTCAAGTCGATGTGAAATCCCCGGGCTTA 604
          || |||||||||||||||||||||||||||| ||||||| ||||||||||||||||
Db   545 TACTGGGCGTAAAGCGTGCGCAGGCGGCCATGCCAAGTCAAGTCAGATGTGAAAGCCCCGGGCTTA 604

Qy   605 ACCTGGGAATTGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCCA 664
          |||||||||| |||||||| ||||| ||||||||| |||||||||| |||||||||
Db   605 ACCTGGGAATTGCGTTTGAAATCGCGTAGAGTGGAGAACACCGGATGGCGAAGGCAGCTCCCTG 664

Qy   665 TGTGTAGCAGTGAAATGCGTAGAGATATGGAGGAACATCGATGGCGAAGGCAGCCCCCTG 724
          ||| |||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db   665 TGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAGCAAACAGGATTAGATACCCTGGT 724

Qy   725 GGTAACCTACGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGT 784
          ||| |||| |||||||||||||||| |||||||||||||||||||||||||||||||
Db   725 GGTTGACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGT 784

Qy   785 AGTCCACGCCGTAAACGATGTCAACTAGTTGTTGGGCCCTTACTA--GGCTTGGTAACGTA 842
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   785 AGTCCACGCCGTAAACTATGTCAACTAGTTGTTCGGATCCTAATTAAGGATTTGGTAACGTA 844

Qy   843 GCTAACGGCGTGAAGTTGACCGCCTGGGGAGTACGTCCGCAGGATTAAAACTCAAAGGAAT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   845 GCTAACGGCGTGAAGTTGACCGCCTGGGGAGTACGTCCGCAAGATTAAAACTCAAAGGAAT 904

Qy   903 TGACGGGGACCCGCACAAGCGGTGGAGTATGTGGATTAATTCGATGCAACGCGGAAAAACC 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   905 TGACGGGGACCCGCACAAGCGGTGGAGTATGTGGATTAATTCGATGCAACGCGAAAAACC 964

Qy   963 TTACCTACCCTTGACATGTAGCGCAATATTTTAGAGATAAAATAGTGCC--TTCGGGAACG 1020
          ||||||||||||||||||||||||| ||| || |||||||||| | ||||||||||||
Db   965 TTACCTACCCTTGACATGCCTGGAATCCTGGAATCATGGGAATCTTAATGAGACACATAAGAGTGCCCGTAAGGGAACC 1024

Qy   1021 CTAACACAGGTGCTGCATGGC-TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1079
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   1025 GGGACACAGGTGCTGCATGGCGTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC 1084

Qy   1080 CGCAACGA---GGCAACCCTTGTCATTAATTGCCAT-CATTTAGTTGGGCACTTTAATG 1135
          ||||||||| ||||||||||||||| || |||| |||||||||||||||||||||
Db   1085 CGCAACGAAGCGCAACCCTTGTCTGTGTTGCTATCCATTTTAATGAGCACTTTAACG 1144

Qy   1136 AGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTAT 1195
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   1145 AGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTC-AGTCCTCATGGCCCTTAT 1203

Qy   1196 GGGTAGGGCTTCACACGTAATACAATGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGG 1255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 GGGTAGGGCTTCACACGTAATACAATGCGCGTACAGAGGGTTGCCAACCCGCGAGGAGG 1263

Qy   1256 AGCTAATCTCAGAAAGCCGTCGTAGTCCGGATCGGAGTCTCGACTCCTGAAG 1315
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 AGCCAATCTCAGAAAGCCGTCGTAGTCCGGATCGGAGTCTCGACTCCGTGAAG 1323

Qy   1316 TCGGAATGCTAGTAATCGCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTA 1375
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   1324 TCGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTA 1383

Qy   1376 CACACCGCCCGTCACACCATGGGAGTGGGTTTCACCAGAAGCAGATAGTCTAACCGTAA- 1434
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CACACCGCCCGTCACACCATGGGAGTGATTTTCACCAGAAGCAGGTAGTCTAACCGCAAG 1443

Qy   1435 GAGGGCGGTTGCCACGGCCGAGATTCATGACTGG 1467
          |||||||||||||||||| |||||||||||||||
Db   1444 GAGGGCGCTTGCCACGTGGGGGGCATGACTGG 1476

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